This Page Is Inserted by IFW Operations and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents will not correct images, please do not report the images to the Image Problems Mailbox.

THIS PAGE BLANK (USPTO)

WORLD INTELLECTUAL PROPERTY ORGANIZATION International Bureau





INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6: C12N 15/29, C07K 14/415, C12N 5/04, 5/14, A01H 5/00, C12N 15/10, 15/82

A2

(11) International Publication Number:

(43) International Publication Date:

WO 99/19492 22 April 1999 (22.04.99)

(21) International Application Number:

PCT/EP98/06977

(22) International Filing Date:

9 October 1998 (09.10.98)

(30) Priority Data:

PO 9745

10 October 1997 (10.10.97)

ΑU

(71) Applicant (for all designated States except US): RHONE-POULENC AGRO [FR/FR]; 14/20, rue Pierre Baizet, F-69009 Lyon (FR).

(72) Inventors; and

- (75) Inventors/Applicants (for US only): DOUTRIAUX, Marie-Pascale [FR/FR]; 64, route de Villebon, F-91160 Saulx les Chartreux (FR). BETZNER, Andreas, Stefan [AU/AU]; 40 Dallachy Place, Page, ACT 2614 (AU). FREYSSINET, Georges [FR/FR]; 21, rue de Nervieux, F-69450 Saint Cyr au Mont d'Or (FR). PEREZ, Pascal [FR/FR]; 17, chemin de la Pradelle, Varennes, F-63450 Chanonat (FR).
- (74) Agent: GENIN, Patrick; Rhône-Poulenc Agro, DPI, 14/20, rue Pierre Baizet, F-69009 Lyon (FR).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR,

KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published

Without international search report and to be republished upon receipt of that report.

(54) Title: METHODS FOR OBTAINING PLANT VARIETIES

(57) Abstract

An isolated and purified DNA molecule comprising a polynucleotide sequence encoding a polypeptide functionally involved in the DNA mismatch repair system of a plant.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	ST	Slovenia
AM	Armenia	Fi	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
ΑÜ	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav	TM	Turkmenistan
BF	Burkina Faso	GR	Greece		Republic of Macedonia	TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	ΙE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of Americ
CA	Canada	ΙT	Italy	MX	Mexico	UZ	Uzhekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	zw	Zimbabwe
CI	Côte d'Ivoire	KP.	Democratic People's	NZ	New Zealand	2	Zimozowe
CM	Carneroon		Republic of Korea	PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ.	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	u	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE '	Estonia	LR	Liberia	SG	Singapore		

10

Methods for Obtaining Plant Varieties

TECHNICAL FIELD

The present invention relates to nucleotide sequences which encode polypeptides involved in the DNA mismatch repair systems of plants, and to the polypeptides encoded by those nucleotide sequences. The invention also relates to nucleotide sequences and polypeptide sequences for use in altering the DNA mismatch repair system in plants. The invention also relates to a process for altering the DNA mismatch repair system of a plant cell, to a process for increasing genetic variations in plants and to processes for obtaining plants having a desired characteristic.

BACKGROUND OF THE INVENTION

Plant breeding essentially relies on and makes use of genetic variation which occurs naturally within and between members of a family, a genus, a species or a subspecies. Another source of genetic variation is the introduction of genes from other organisms which may or may not be related to the host plant.

Allelic loci or non-allelic genes which constitute or contribute to desired quantitative (e.g. growth performance, yield, etc.) or qualitative (e.g. deposition, content and composition of seed storage products; pathogen resistance genes: etc.) traits that are absent, incomplete or inefficient in a species or subspecies of interest are typically introduced by the plant breeder from other species or subspecies, or de novo. This introduction is often done by crossing, provided that the species to be crossed are sexually compatible. Other means of introducing genomes, individual chromosomes or genes into plant cells or plants are well known in the art. They include cell fusion, chemically aided transfection (Schocher et al., 1986, Biotechnology 4: 1093) and ballistic (McCabe et al., 1988, Biotechnology 6: 923), microinjection (Neuhaus et al., 1987, TAG 75: 30), electroporation of protoplasts (Chupeau et al., 1989, Biotechnology 7: 53) or microbial transformation methods such as Agrobacterium mediated transformation (Horsch et al., 1985, Science 227: 1229; Hiei et al., 1996, Biotechnology 14: 745).

However, when a foreign genome, chromosome or gene is introduced into a plant, it will often segregate in subsequent generations from the genome of the recipient plant or plant cell during mitotic and meiotic cell divisions and, in consequence, become lost from the host plant or plant cell into which it had been introduced. Occasionally, however, the introduced genome, chromosome or gene physically combines entirely or in part with the genome, chromosome or gene of the host plant or plant cell in a process which is called recombination.

Recombination involves the exchange of covalent linkages between DNA molecules in regions of identical or similar sequence. It is referred to here as homologous recombination if donor and recipient DNA are identical or nearly identical (at least 99%)

hase sequence identity), and as homeologous recombination if donor and recipient DNA are not identical but are similar (less than 99% base sequence identity).

The ability of two genomes, chromosomes or genes to recombine is known to depend largely on the evolutionary relation between them and thus on the degree of sequence similarity between the two DNA molecules. Whereas homologous recombination is frequently observed during mitosis and meiosis, homeologous recombination is rarely or never seen.

From a breeder's perspective, the limits within which homologous recombination occurs, therefore, define a genetic barrier between species, varieties or lines, in contrast to homeologous recombination which can break this barrier. Homeologous recombination is thus of great importance for plant breeding. Accordingly there is a need for a process for enhancing the frequency of homeologous recombination in plants. In particular, there is a need for a process of increasing homeologous recombination to significantly shorten the length of breeding programs by reducing the number of crosses required to obtain an otherwise rare recombination event.

At least in Escherichia coli, homologous and homeologous recombination are known to share a common pathway that requires among others the proteins RecA, RecB, RecC. RecD and makes use of the SOS induced RuvA and RuvB, respectively. It has been suggested that mating induced recombination follows the Double-Strand Break Repair 20 model (Szostak et al., 1983, Cell 33, 25-35), which is widely used to describe genetic recombination in eukaryotes. Following the alignment of homologous or homeologous DNA double helices the RecA protein mediates an exchange of a single DNA strand from the donor helix to the aligned recipient DNA helix. The incoming strand screens the recipient helix for sequence complementarity, seeking to form a heteroduplex by hydrogen 25 bonding the complementary strand. The displaced homologous or homeologous strand of the recipient helix is guided into the donor helix where it base pairs with its counterpart strand to form a second heteroduplex. The resulting branch point then migrates along the aligned chromosomes thereby elongating and thus stabilising the initial heteroduplexes. Single stranded gaps (if present) are closed by DNA synthesis. The strand cross overs 30 (Holliday junction) are eventually resolved enzymatically to yield the recombination products.

Although in wild type E. coli homologous and homeologous recombination are thus mechanistically similar if not identical, homologous recombination in conjugational crosses E. coli x E. coli occurs five orders of magnitude more frequently than homeologous recombination in conjugational crosses E. coli x S. typhimurium (Matic et al. 1995; Cell 80, 507-515). The imbalance in favour of homologous recombination was shown to be caused largely by the bacterial MisMatch Repair (MMR) system since its

inactivation increased the frequency of homeologous recombination in E. coli up to 1000 fold (Rayssiguier et al. 1989, Nature 342, 396-401).

In E. coli, the MMR system (reviewed by Modrich 1991, Annual Rev Genetics 25, 229-253) is composed of only three proteins known as MutS, MutL and MutH. MutS recognizes and binds to base pair mismatches. MutL then forms a stable complex with mismatch bound MutS. This protein complex now activates the MutH intrinsic single stranded endonuclease which nicks the strand containing the misplaced base and thereby prepares the template for DNA repair enzymes.

During recombination, MMR components inhibit homeologous recombination. In vitro experiments demonstrated that MutS in complex with MutL binds to mismatches at the recombination branch point and physically blocks RecA mediated strand exchange and heteroduplex formation (Worth et al., 1994; PNAS 91, 3238-3241). Interestingly, the SOS dependent RuvAB mediated branch migration is insensitive to MutS/MutL, explaining the observed slight increase in SOS dependent homeologous recombination.

15 Homeologous mating even induces the SOS response, thereby taking advantage of RuvAB induction (Matic et al. 1995, Cell 80, 507-515).

The MMR system thus appears to be a genetic guardian over genome stability in E. coli. In this role it essentially determines the extent to which genetic isolation, that is, speciation, occurs. The diminished sensitivity of the SOS system to MMR, however, allows (within limits) for rapid genomic changes times of stress, providing the means for fast adaptation to altered environmental conditions and thus contributing to intraspecies genetic variation and species evolution.

The important role of MMR in preserving genomic integrity has been established also in certain eukaryotes. In its efficiency, the human MMR, for example, may even counteract potential gene therapy tools such as triple-helix forming oligonucleotides including RNA-DNA hybrid molecules (Havre et al., 1993, J. Virology 67: 7234-7331; Wang et al., 1995, Mol. Cell. Biol. 15: 1759-1768; Kotani et al., 1996, Mol. Gen. Genetics 250: 626-634; Cole-Strauss et al., 1996, Science 273: 1387-1389). Such oligonucleotides are designed to introduce single base changes into selected DNA target sequences in order to inactivate for example cancer genes or to restore their normal function. The resulting base mismatches however are recognised by the mismatch repair system which then directs removal of the mismatched base, thereby reducing the efficiency of oligonucleotide induced site-specific mutagenesis.

To date, two families of related genes, homologous to the bacterial MutS and MutL genes have been identified or isolated in yeast and mammals (recent reviews by Arnheim and Shibata, 1997, Curr. Opinion Genet. Dev. 7, 364-370; Modrich and Lahue, 1996, Annual Rev. Biochem. 65, 101-133; Umar and Kunkel, 1996, Eur. J. Biochem. 238, 297-307). Biochemical and genetic analysis indicated that eukaryotic MutS homologs (MSH)

and MutL homologs (MLH, PMS), respectively, fulfil similar protein functions as their bacterial counterparts. Their relative abundance, however, could reflect different mismatch specificity and/or specialisation for different tissues or organelles or developmental processes such as mitotic versus meiotic recombination.

To date, six different genes homologous to *MutS* have been isolated in yeast (yMSH), and their homologs have been found in mouse (mMSH) and human (hMSH), respectively. Encoded proteins yMSH2, yMSH3 and yMSH6 appear to be the main MutS homologs involved in MMR during mitosis and meiosis in yeast, where the complementary proteins MSH3 and MSH6 alternatively associate with MSH2 to recognise different mismatch substrates (Masischky et al., 1996, Genes Dev. 10, 407-420). Similar protein interactions have been demonstrated for the human homologs hMSH2, hMSH3 and hMSH6 (Acharya et al., 1996, PNAS 93, 13629-13634).

MutL homologs (MLH and PMS), recently reviewed by Modrich and Lahue (1996, Annual Rev. Biochem. 65. 101-133) have so far been found in yeast (yMLH1 and yPMS1), mouse (mPMS2) and human (hMLH1, hPMS1 and hPMS2). The hPMS2 is a member of a family of at least 7 genes (Horii et al., 1994, Biochem. Biophys. Res. Commun. 204, 1257-1264) and its gene product is most closely related to yPMS1. Prolla et al. (1994, Science 265, 1091-1093) presented evidence for yPMS1 and yMLH1 to physically associate with each other and, together, to interact with the MutS homolog yMSH2 to form a ternary complex involved in mismatch substrate binding.

However, while medical interest in mismatch repair has prompted extensive research on MMR in bacteria, yeast and mammals, MMR genes have not been isolated from higher plants prior to the present invention and no attempts to adjust the plant MMR to plant breeding needs have been reported.

SUMMARY OF THE INVENTION

According to a first embodiment of the invention, there is provided an isolated and purified DNA molecule comprising a polynucleotide sequence encoding a polypeptide functionally involved in the DNA mismatch repair system of a plant. In one form of this embodiment, the invention provides an isolated and purified DNA molecule comprising a polynucleotide sequence encoding a polypeptide which is homologous to a mismatch repair polypeptide of a yeast or of a human. More particularly, the invention provides polynucleotide sequences encoding polypeptides which are homologous to the mismatch repair polypeptides MSH3 and MSH6 of Saccharomyces cerevisiae. Still more particularly, the invention provides the coding sequences of the genes AtMSH3 and AtMSH6 of Arabidopsis thaliana. as defined hereinbelow, and polynucleotide sequences encoding polypeptides which are homologous to polypeptides encoded by AtMSH3 and AtMSH6.

25

According to a second embodiment of the invention, there is provided an isolated and purified polypeptide functionally involved in the DNA mismatch repair system of a plant, for example a polypeptide which is homologous to a mismatch repair polypeptide of a yeast or of a human such as a polypeptide encoded by the genes AtMSH3 or AtMSH6 of 5 Arabidopsis thaliana, as defined hereinbelow.

According to a third embodiment of the invention, there is provided an isolated and purified DNA molecule comprising a polynucleotide sequence selected from the group consisting of (i) a sequence encoding a polynucleotide which is capable of interfering with the expression of a plant polynucleotide sequence encoding a polypeptide which is homologous to a mismatch repair polypeptide of a yeast or of a human and thereby disabling said plant polynucleotide sequence; and (ii) a sequence encoding a polypeptide capable of disrupting the DNA mismatch repair system of a plant.

According to a fourth embodiment of the invention there is provided a chimeric gene comprising a DNA sequence selected from the group consisting of (i) a sequence encoding a polynucleotide which is capable of interfering with the expression of a plant polynucleotide sequence encoding a polypeptide which is homologous to a mismatch repair polypeptide of a yeast or of a human and thereby disabling said plant polynucleotide sequence, and (ii) a sequence encoding a polypeptide capable of disrupting the DNA mismatch repair system of a plant: together with at least one regulation element capable of functioning in a plant cell. Examples of such regulation elements include constitutive, inducible, tissue type specific and cell type specific promoters such as 35S. NOS, PR1a, AoPR1 and DMC1. Typically, a chimeric gene of the fourth embodiment will also include at least one terminator sequence, more typically exactly one terminator sequence.

In the third and fourth embodiments, said interference, by said polynucleotide sequence, with the expression of a plant polynucleotide sequence encoding a polypeptide which is homologous to a mismatch repair peptide of a yeast or a human typically occurs by hybridisation or by co-suppression.

According to a fifth embodiment of the invention there is provided a plasmid or vector comprising a chimeric gene of the fourth embodiment. A vector of the fifth 30 embodiment may be, for example, a viral vector or a bacterial vector.

According to a sixth embodiment of the invention, there is provided a plant cell stably transformed, transfected or electroporated with a plasmid or vector of the fifth embodiment.

According to seventh embodiment of the invention, there is provided a plant 35 comprising a cell of the sixth embodiment.

According to an eighth embodiment of the invention, there is provided a process for at least partially inactivating a DNA mismatch repair system of a plant cell, comprising

transforming or transfecting said plant cell with a DNA sequence of the third embodiment or a chimeric gene of the fourth embodiment or a plasmid or vector of the fifth embodiment, and causing said DNA sequence to express said polynucleotide or said polypeptide.

According to a ninth embodiment of the invention, there is provided a process for increasing genetic variation in a plant comprising obtaining a hybrid plant from a first plant and a second plant, or cells thereof, said first and second plants being genetically different; altering the mismatch repair system in said hybrid plant; permitting said hybrid plant to self-fertilise and produce offspring plants; and screening said offspring plants for plants in which homeologous recombination has occurred. For example, homeologous recombination may be evidenced by new genetic linkage of a desired characteristic trait or of a gene which contributes to a desired characteristic trait.

According to a tenth embodiment of the invention there is provided a process for obtaining a plant having a desired characteristic, comprising altering the mismatch repair system in a plant, cell or plurality of cells of a plant which does not have said desired characteristic, permitting mutations to persist in said cells to produce mutated plant cells, deriving plants from said mutated plant cells, and screening said plants for a plant having said desired characteristic.

In a preferred form of the ninth and tenth embodiments of the invention, the step of altering the mismatch repair system comprises introducing into said hybrid plant, plant, cell or cells a chimeric gene of the fourth embodiment and permitting the chimeric gene to express a polynucleotide which is capable of interfering with the expression of a plant polynucleotide sequence in a mismatch repair gene of the hybrid plant, plant, cell or cells, or a polypeptide capable of disrupting the DNA mismatch repair system of the hybrid plant or cells.

In other embodiments, the invention provides (a) an oligonucleotide capable of hybridising at 45°C under standard PCR conditions to a DNA molecule of the first embodiment; (b) an oligonucleotide capable of hybridising at 45°C under standard PCR conditions to the DNA of SEQ ID NO: 18 and (c) an oligonucleotide capable of hybridising at 45°C under standard PCR conditions to the DNA of SEQ ID NO:30; with the proviso that the oligonucleotide of (a), (b) and (c) is other than SEQ ID NO:1 or SEQ ID NO:2.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides a diagrammatic representation of the primer sequences used to 35 isolate AtMSH3.

Figure 2 is a plasmid map of clone 52, showing restriction enzyme cleavage sites in the 5' half of the full-length cDNA for AtMSH3.

Figure 3 is a plasmid map of clone 13, showing restriction enzyme cleavage sites in the 3' half of the full-length cDNA for AtMSH3.

Figure 4 is a sequence listing of the coding sequence of AtMSH3, together with a deduced sequence of the encoded polypeptide.

Figure 5 is a protein alignment of yeast (Saccharomyces cerevisiae) and Arabidopsis thaliana MSH3 protein.

Figure 6 provides a diagrammatic representation of the primer sequences used to isolate AtMSH6.

Figure 7 is a plasmid map of clone 43, showing restriction enzyme cleavage sites in the 5' half of the full-length cDNA for AtMSH6.

Figure 8 is a plasmid map of clone 62, showing restriction enzyme cleavage sites in the 3' half of the full-length cDNA for AtMSH6.

Figure 9 is a sequence listing of the coding sequence of AtMSH6, together with a deduced sequence of the encoded polypeptide.

Figure 10 is a protein alignment of yeast (Saccharomyces cerevisiae) and Arabidopsis thaliana MSH6 protein.

Figure 11 is a genomic sequence listing of AtMSH6.

Figure 12 is a plasmid map of plasmid pPF13.

Figure 13 is a plasmid map of plasmid pPF14.

Figure 14 is a plasmid map of plasmid pCW186.

Figure 15 is a plasmid map of plasmid pCW187.

Figure 16 is a plasmid map of plasmid pPF66.

Figure 17 is a plasmid map of plasmid pPF57.

Figure 18 is a diagrammatic representation of an antisense gene construction for use in homeologous meiotic recombination.

Figure 19 is a plasmid map of plasmid p3243.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is based on the inventors' discovery that there exist in higher plants genes which are homologous to MMR genes in E. coli, and to MMR genes in yeasts and humans.

Thus, the inventors have identified genes, herein designated AtMSH3 and AtMSH6, of the plant Arabidopsis thaliana which encode the proteins AtMSH3 and AtMSH6. These plant proteins are homologous to yMSH3 and yMSH6, respectively. The present inventors have isolated cDNAs encoding the proteins AtMSH3 and AtMSH6 and have isolated the complete gene encoding AtMSH6. Given the teaching herein, other genes (for example AtMSH2, and genes of other plants) may be obtained which are involved in DNA mismatch repair in plants, including other genes which encode polypeptides homologous to MMR proteins of yeasts or humans, such as genes which encode

20

WO 99/19492 PCT/EP98/06977

polypeptides homologous to yeast MSH2. MLH1 or PMS2, or to human MLH1. PMS1 or PMS2. For example, given the teaching herein, genes of members of the *Brassicaceae* family or of other unrelated families, for example the *Poaceae*, the *Solanaceae*, the *Asteraceae*, the *Malvaceae*, the *Fabaceae*, the *Linaceae*, the *Canabinaceae*, the *Dauaceae* and the *Cucurbitaceae* family, and which encode polypeptides homologous to MMR proteins of yeasts or humans may be obtained.

Examples of plants whose genes encoding polypeptides homologous to MMR proteins of yeasts or humans may be obtained given the teaching herein include maize, wheat, oats, barley, rice, tomato, potato, tobacco, capsicum, sunflower, lettuce, artichoke, safflower, cotton, okra, beans of many kinds including soybean, peas, melon, squash, cucumber, oilseed rape, broccoli, cauliflower, cabbage, flax, hemp, hops and carrot.

Within the meaning of the present invention, a first polypeptide is defined as homologous to a second polypeptide if the amino acid sequence of the first polypeptide exhibits a similarity of at least 50% on the polypeptide level to the amino acid sequence of the second polypeptide.

A procedure which may be followed to obtain genes AtMSH3 and AtMSH6 is described in Example 1. Essentially the same technique may be applied to obtain other mismatch repair genes of Arabidopsis thaliana, and essentially the same technique as 20 exemplified herein may be applied to cDNA obtained by reverse transcription of RNA from other plants. Alternatively, given the sequence information disclosed herein, other degenerate oligonucleotide primers, especially oligonucleotides of the invention which are capable of hybridising at 45°C under standard PCR conditions (such as the conditions described in Example 1 using primers UPMU and DOMU) to AtMSH3 and/or AtMSH6 25 may be designed and obtained for use in isolating sequences of plant mismatch repair genes which are homologous to AtMSH3 or AtMSH6, from other plants. oligonucleotides of the invention which are capable of hybridising at 45°C under standard PCR conditions to plant mismatch repair genes of plants other than Arabidopsis thaliana also fall within the scope of the present invention and may be utilised to obtain mismatch Typically, such oligonucleotides are capable of 30 repair genes of still other plants. hybridising at 45°C under standard PCR conditions to a DNA molecule which encodes a polypeptide which is homologous to a mismatch repair polypeptide of a yeast or a human. The temperature at which oligonucleotides of the invention hybridise to AtMSH3 and/or AtMSH6, or to plant mismatch repair genes of plants other than Arabidopsis thaliana, or 35 to DNA molecules which encode polypeptides which are homologous to a mismatch repair polypeptide of a yeast or a human may be higher than 45°C, for example at least 50°C, or at least 55°C, or at least 60°C or as high as 65°C.

The successful gene isolation disclosed herein demonstrates for the first time the existence of MMR in higher plants and indicates the presence of other plant MMR genes. For example, genes encoding the plant homologs of MSH1, MSH2, MSH4, MSH5, PMS1, PMS2 and MLH1 may be identified given the teaching herein. Such genes, as well as those specifically described herein, separately or in combination, are useful in manipulating the plant MMR for plant breeding purposes. Thus, for example, the plant MMR may be altered by including in a plant cell a polynucleotide sequence as defined herein above with reference to the third embodiment of the invention, and causing the polynucleotide sequence to express either a polynucleotide which disables a plant MMR genes.

The DNA molecule of the third embodiment of the invention includes a polynucleotide sequence (herein referred to as a MMR altering gene) which may for example encode sense, antisense or ribozyme molecules characterised by sufficient base sequence similarity or complementarity to the gene to be altered to permit the antisense or 15 ribozyme molecule to hybridise with the plant MMR gene in vivo or to permit the sense molecule to participate in co-suppression. Alternatively, the MMR altering gene may encode a protein or proteins which interfere with the activity of a plant MMR protein and thus disrupt the plant's MMR system. For example, such encoded proteins may be antibodies or other proteins capable of interfering with MMR protein function, such as by 20 complexing with a protein functionally involved in plant MMR thereby disrupting the MMR of the plant. An example of such a protein is the MSH3 protein of Arabidopsis thaliana described herein or a protein of another plant which is homologous to the MSH3 protein of A. thaliana. For instance, overexpression of MSH3 in a plant cell causes MSH2 present in the cell to be substantially completely complexed, disrupting the 25 mismatch repair mechanism or mechanisms in the cell which are functionally dependent Similarly, mismatch repair on the presence of a complex of MSH2 with MSH6. mechanisms which depend on the presence of a complex of MSH2 and MSH3 may be disrupted by the overexpression of MSH6.

A chimeric gene of the fourth embodiment, incorporating a MMR altering gene, may be prepared by methods which are known in the art. Similarly, the MMR altering gene may be introduced into a plant cell, regenerating tissue or whole plant by techniques known in the art as being suitable for plant transformation, or by crossing. Known transformation techniques include Agrobacterium tumefaciens or A. rhizogenes mediated gene transfer, ballistic and chemical methods, and electroporation of protoplasts.

The MMR altering gene or genes are typically expressed from suitable promoters. Suitable promoters may direct constitutive expression, such as the 35S or the NOS promoter. Usually, however, the promoter will direct either inducible or tissue specific (e.g. callus; embryonic tissue; etc.), cell type specific (e.g. protoplasts; meiocytes; etc.) or developmental (e.g. embryo) expression of the altering gene or genes, in order for the

MMR system to function in tissue types or cell types, or at developmental stages of the plant, in which it is not desirable for the MMR system to be altered. Using such promoters, therefore, the activity of a MMR altering gene may be limited to a specific stage during plant development or it may be altered by controlling conditions external to the plant, and the deleterious effects of a permanently disabled or altered DNA mismatch repair system in a plant may be avoided. Examples of suitable promoters which are not constitutive are known in the art and include inducible promoters such as PR1a (reviewed by Gatz, 1997, Annual Rev. Plant Phys. Plant Mol. Biol. 48: 89), tissue specific promoters such as AoPR1 (Sabahattin et al., 1993, Biotechnology 11: 218), and cell-type specific promoters such as DMC1.

A chimeric gene in accordance with the invention may further be physically linked to one or more selection markers such as genes which confer phenotypic traits such as herbicide resistance, antibiotic resistance or disease resistance, or which confer some other recognisable trait such as male sterility, male fertility, grain size, colour, growth rate, flowering time, ripening time, etc.

The process of the tenth embodiment of the invention provides, for example, a process for generating intraspecies genetic variation by altering the mismatch repair system in a plant cell, in regenerating plant tissue or in a whole plant. The plant cell, regenerating tissue or whole plant includes and expresses one or more MMR altering 20 genes which are capable of altering mismatch repair in the plant cell, regenerating tissue or whole plant. Alteration of MMR may be achieved, for example, by inactivating the genes encoding plant MSH3 and/or plant MSH6. It is preferred to inactivate the plant MSH3 and MSH6 encoding genes at the same time and in the same plant cell, regenerating tissue or whole plant. Typically in this preferred form of the invention 25 inactivation of either plant MSH3 or MSH6 alone is insufficient to substantially alter the plant's mismatch repair system and only when both MSH3 and MSH6 are inactivated simultaneously is the plant's mismatch repair system sufficiently altered to prevent the MMR system from recognising base pair mismatches, base insertions or deletions as a result of DNA replication errors, DNA damage, or oligonucleotide induced site-specific 30 mutagenesis. However, in some applications of the invention, inactivation of only one gene may also be used to cause genomic instability or increase the efficiency of sitespecific mutagenesis.

If desired, the MMR altering gene or genes may later be rendered non-functional or ineffective, or may be removed from the genome of the plant cell, regenerating tissue or whole plant in order to restore mismatch repair in the plant cell, regenerating tissue or whole plant. The MMR altering gene or genes may be inactivated by means of known gene inactivation tools, such as ribozymes, or may be removed from the genome using gene elimination systems known in the art, such as CRE/LOX. It is preferred to render two genes, whose gene products combine to incapacitate MMR, ineffective by separating

the altering genes through segregation. Therefore, in a preferred embodiment of the invention a first plant cell or plant is generated in which only plant MSH3 is incapacitated, and a second plant cell or plant is generated in which only plant MSH6 is incapacitated. The combination of both genomes, for example by crossing, then produces significant MMR deficiency in those cells or plants which have inherited both altering genes. If the altering genes are expressed from unlinked loci, gene segregation restores MMR activity in the progeny of the cells or plants.

In a process of the ninth embodiment of this invention, homeologous recombination is enhanced between different genomes, chromosomes or genes in plant cells or plants by altering MMR in said plant cells or plants. Such genomes, chromosomes or genes are characterised in that they originate from different plant families, genera, species, subspecies, plant varieties or lines. Hybrid plant cells or hybrid plants may be produced by crossing, by cell fusion or by other techniques known in the art. These plant cells or plants are further characterised by expressing one or more genes that are capable of altering mismatch repair in the plant cell or plants.

In the process of the ninth embodiment, the homeologous recombination is typically for the purpose of introducing a desired characteristic in the hybrid plant. In this typical application of the process of the ninth embodiment, and in the process of the tenth embodiment the desired characteristic may be any characteristic which is of value to the plant breeder. Examples of such characteristics are well known in the art and include altered composition or quality of leaf or seed derived storage products (e.g. oil, starch, protein), altered composition or quality of cell walls (e.g. decrease in lignin content), altered growth rate, prolonged flowering, increased plant yield or grain yield, altered plant morphology, resistence to pathogens, tolerance to or improved performance under environmental stresses of various kinds, etc.

In a preferred form of the tenth embodiment, an MMR altering gene is cointroduced along with the homeologous genome, chromosome or gene of another plant
cell or plant into an MMR proficient plant cell or MMR proficient plant to produce a
hybrid plant cell or hybrid plant in which homeologous recombination can occur.

Suitably, the MMR proficient plant cell or MMR proficient plant may also include an
MMR altering gene. For example a gene capable of inactivating plant MSH3 may be cointroduced along with the homeologous genome, chromosome or gene of another plant
cell or plant into an MMR proficient plant cell or MMR proficient plant in which MSH6
is inactivated. A resultant hybrid plant in which homeologous recombination occurs will
include both the MSH3 and MSH6 altering genes and its MMR system will therefore be
inactivated.

In this form of the invention, if hybrid plants are to be produced by crossing, the MMR altering gene preferably originates from the male parent, thus ensuring that the

MMR altering gene is always introduced and is not present in the recipient cell. That is, the MMR of the recipient cell, prior to introduction of the MMR altering gene, is typically proficient. Alternatively, if an MMR altering gene is present in a recipient cell it may be ineffective or inefficient on its own, or it may be linked to an inducible or tissue specific or cell type specific promoter which only renders the MMR altering gene active under limited conditions.

Thus, in a preferred form of the process of the ninth embodiment, the MMR system of the hybrid plant is initially unaltered. In this form of the process, the step of altering the mismatch repair system may comprise introducing into the hybrid plant, or cells thereof, a MMR altering gene, such as by Agrobacterium tumefaciens or A. rhizogenes mediated gene transfer, ballistic and chemical methods, and electroporation of protoplasts.

The MMR altering gene or genes are typically expressed from suitable promoters, as described above. Preferably, the promoter is transcriptionally active in mitotically and meiotically active tissue and/or cells to ensure MMR alteration after chromosome pairing at mitosis and meiosis, respectively. The preferred timing for MMR alteration is at meiosis, because recombinant genomes, chromosomes or genes are directly transmitted to the progeny. A suitable meiocyte specific promoter is for example the DMC1 promoter from Arabidopsis thaliana ssp. Ler. (Klimyuk and Jones, 1997, Plant J. 11, 1-14). However, mitotic homeologous recombination is also a desirable outcome as somatic recombination events can be transmitted to offspring due to the totipotency of plant cells and the lack of predetermined germ cells in plants.

If desired, the MMR altering gene or genes may later be rendered non-functional or ineffective, or may be removed from the hybrid plant or hybrid plant cells, in order to restore mismatch repair in the hybrid plant or hybrid plant cells. The MMR altering gene or genes may be inactivated by means of known gene inactivation tools as described herein above.

EXAMPLES

Example 1. Cloning of the AtMSH3 and AtMSH6 coding sequences

Isolation of partial AtMSH3 and AtMSH6 consensus sequences

Degenerate oligonucleotides UPMU (SEQ ID NO:1) and DOMU (SEQ ID NO:2)

UPMU CTGGATCCACIGGICCIAA(C/T)ATG

DOMU CTGGATCC(A/G)TA(A/G)TGIGTI(A/G)C(A/G)AA

were used to isolate AtMSH3 and AtMSH6 sequences by PCR amplification.

Primers UPMU and DOMU correspond to conserved amino acid sequences of the proteins MutS (E. coli and S. typhimurium), HexA (S. pneumoniae). Repl (mouse) and Ducl (human). The conserved regions to which they are targeted are TGPNM for UPMU (amino acid positions 852-856 for AtMSH6 and 816-820 for AtMSH3) FATHY or FVTHY

for DOMU (amino acid positions 964-968 for AtMSH6 and 928-932 for AtMSH3, respectively.) These primers have been used to isolate MSH2 and MSH1 from yeast (Reenan and Kolodner, Genetics 132: 963-973 (1992)) and MSH2 from *Xenopus* and mouse (Varlet et al., Nuc. Acids Res. 22:5723-5728 (1994)).

Template single strand cDNA was produced by reverse transcription of 2 µg total RNA from a cell suspension culture of Arabidopsis thaliana ecotype Columbia (Axelos et al. 1989, Mol. Gen. Genetics 219: 106-112). The PCR reaction was performed under the following conditions in a final volume of 100µl: 0.2mM dNTP, 1µM each primer, 1XPCR buffer, lu Taq DNA polymerase (Appligene) in the presence of template cDNA. PCR 10 parameters were 5 minutes at 94°C, followed by 30 cycles of 40 seconds at 95°C, 90 seconds at 45°C, 1 minute at 72°C. The amplification products were cloned into pGEM-T vector (Promega) and sequenced. Two different clones were isolated, S5 (350bp) was homologous to MSH3, S8 (327bp) was homologous to MSH6. Complete cDNA sequences were then isolated according to the Marathon cDNA amplification kit procedure (Clontech). 15 In summary, this procedure involves producing double stranded cDNA by reverse transcription of 2µg polyA+ RNA from the cell suspension culture of Arabidopsis. Adaptors are ligated on each side of the cDNA. The ligated cDNA is used as a template for 5' and 3' RACE PCR reactions in the presence of primers that are specific for the adaptor on one side (AP1 and AP2), and specific for the targeted gene on the other side. A 5' and a 3' 20 fragment that overlap are thus produced for each gene. The complete gene coding sequence can be reconstituted taking advantage of a unique restriction site, if available, in the overlapping region. Specific details of this procedure as it was used to isolate AtMSH3 and AtMSH6 coding regions, are as follows.

Isolation of AtMSH3 complete coding sequence

From the sequence of clone S5, primer 636 (SEQ ID NO:3) was designed:

TGCTAGTGCCTCTTGCAAGCTCAT.

Primer AP1 (SEQ ID NO:4) is complementary to a portion of an adaptor sequence which had been ligated to the 5' and 3' ends of Arabidopsis cDNA:

API CCATCCTAATACGACTCACTATAGGGC.

PCR performed on the ligated cDNA with primers 636 and AP1 for the 5' RACE PCR was followed by a second round of amplification with the nested primers AP2 (SEQ ID NO:5) and S525 (SEQ ID NO:6)

AP2 ACTCACTATAGGGCTCGAGCGGC

S525 AGGTTCTGATTATGTGTGACGCTTTACTTA

35 (the latter was also designed to correspond to a part of the sequence of clone S5) and produced a 2720bp DNA fragment. Figure 1 provides a diagrammatic representation of the primer sequences used to isolate AtMSH3. Another primer (S51, SEQ ID NO:7)

S51 GGATCGGGTACTGGGTTTTGAGTGTGAGG

25

was designed closer to the 5' border and permitted the determination of 99bp upstream to the ATG initiation codon. For the 3' RACE PCR, a first PCR reaction was performed with primers AP1 and 635 (SEQ ID NO:8).

- 635 GCACGTGCTTGATGGTGTTTTCAC
- 5 followed by a second round of amplification, using the nested primers AP2 and S523 (SEQ ID NO:9)
- which produced a DNA fragment of 890bp. Both DNA fragments were subcloned into pGEM-T and sequenced. Since PCR amplification using the Expand Long Template PCR 10 System (Boehringer-Mannheim) produced errors in the sequence, new oligonucleotides were designed to isolate those sequences again by PCR, but with the high fidelity DNA polymerase Pfu. PCR with primers 1S5 (SEQ ID NO:10) and S53 (SEQ ID NO:11)
 - 1S5 ATCCCGGGATGGGCAAGCAAAAGCAGCAGACGA
 - S53 GACAAAGAGCGAAATGAGGCCCCTTGG
- amplified the 1244bp fragment clone 52 (SEQ ID NO:12, cloned into pUC18/Sma1). PCR with primers S52 (SEQ ID NO:13) and 2S5 (SEQ ID NO:14)
 - 2S5 ATCCCGGGTCAAAATGAACAAGTTGGTTTTAGTC
 - S52 GCCACATCTGACTGTTCAAGCCCTCGC

amplified the 2104bp clone 13 (SEQ ID NO:15, cloned into pUC18/Sma1). The complete coding sequence of the AtMSH3 gene was reconstructed in pUC18 by ligating the 5' half of AtMSH3 (clone 52) to the 3' half of AtMSH3 (clone 13) after digesting with BamH1 which has a unique cleavage site in the overlapping region of both clones. This manipulation yielded plasmid pPF26. The Smal fragment from pPF26 contains the complete AtMSH3 coding sequence. The remaining primers referred to in Figure 1 are as follows:

- S51 GGATCGGGTACTGGGTTTTGAGTGTGAGG (SEQ ID NO:16)
- S525 AGGTTCTGATTATGTGTGACGCTTTACTTA (SEQ ID NO:17)

Figures 2 and 3 provide plasmid maps of clones 52 and 13 respectively, showing restriction enzyme cleavage sites. The complete AtMSH3 coding sequence (SEQ ID NO:18) 30 is 3246bp long and is shown in Figure 4 together with the deduced sequence (SEQ ID NO:19) of the encoded polypeptide. AtMSH3 is clearly homologous to the yeast and mouse MSH3 genes. A sequence alignment of polypeptides encoded by AtMSH3 and that encoded by Saccharomyces cerevisiae MSH3 is set out in Figure 5.

Isolation of the AtMSH6 complete coding sequence and genomic sequences

- The same procedure allowed isolation of the AtMSH6 cDNA. Figure 6 provides a diagrammatic representation of the primer sequences used to isolate AtMSH6. For the 5 RACE PCR, primers 638 (SEQ ID NO:20) and AP1 (SEQ ID NO:4)
 - 638 TCTCTACCAGGTGACGAAAAACCG
 allowed the amplification of a 2889 DNA fragment. Primer S81 (SEQ ID NO:21)

S81 CGTCGCCTTTAGCATCCCCTTCCTTCAC

helped define the 142bp upstream to the ATG initiation codon. On the 3' side, RACE PCR was initially performed with primers S823 (SEQ ID NO:22) and AP1 (SEQ ID NO:4).

S823 GCTTGGCGCATCTAATAGAATCATGACAGG

5 and then with the nested primers 637 (SEQ ID NO:23) and AP2 (SEQ ID NO:5).

637 GACAGCGTCAGTTCTTCAGAATGC

to produce a 774bp DNA fragment. As for AtMSH3, those fragments were cloned and sequenced. Re-isolation of the DNA sequence using the high fidelity Pfu polymerase and newly designed primers 1S8 (SEQ ID NO:24) and S83 (SEQ ID NO:25) (for the 5° side) led to a 2182 bp DNA fragment identified as clone 43 (SEQ ID NO:26, cloned in pUC18/Sma1), and a 1379bp clone identified as clone 62 (SEQ ID NO:27, also cloned in pUC18/Sma1).

1S8 ATCCCGGGATGCAGCGCCAGAGATCGATTTTGT

2S8 ATCCCGGGTTATTTGGGAACACAGTAAGAGGATT (SEQ ID

NO:28)

15

S82 GCGTTCGATCATCAGCCTCTGTGTTGC (SEQ ID NO:29)

S83 CGCTATCTATGGCTGCTTCGAATTGAG

Figures 7 and 8 provide plasmid maps of clones 43 and 62 respectively, showing restriction enzyme cleavage sites. Clones 43 and 62 were digested by the Xmn1 restriction enzyme for which a unique site is present in their overlapping region and then ligated. The complete AtMSH6 coding sequence (SEQ ID NO:30) is 3330bp long and is shown in Figure 9 together with the deduced sequence (SEQ ID NO:31) of the encoded polypeptide. AtMSH6 is clearly homologous to the yeast and mouse MSH6genes. A sequence alignment of polypeptides encoded by AtMSH6 and that encoded by Saccharomyces cerevisiae MSH6 is set out in Figure 10.

An AtMSH6 genomic sequence was also isolated from a genomic DNA library constituted after partial Sau3Al digestion of DNA from the Arabidopsis cell suspension. 8062bp were sequenced that covered the AtMSH6 gene and show colinearity with the cDNA. 16 introns are found scattered along the gene. The complete genomic sequence 30 (SEQ ID NO:98) is shown in Figure 11.

Example 2. A measure of somatic variation in MMR deficient plants

Constructs

Constructs with antisense AtMSH3 or antisense AtMSH6 or both AtMSH3/AtMSH6 under the control of a single 35S promoter have been inserted into the binary vector pPZP121 (Hajdukiewicz et al., Plant Mol. Biol. 23, 793-799) between the right and left borders of the T-DNA. The pPZP121 plasmid confers chloramphenicol resistance to Escherichia coli or Agrobacterium tumefaciens bacteria. The aacC1 gene is carried by the T-DNA and allows selection of transformed plant cells on gentamycin (Hajdukiewicz et al., Plant Mol. Biol. 25, 989-994). For the purpose of expressing antisense constructs, a 35S

promoter/terminator cassette with a polylinker was introduced into pPZP121. The 3' ends of the considered genes have been chosen since this region seems more efficient for antisense inhibition. For AtMSH3 this corresponds to clone 13 (2104bp), for AtMSH6 this corresponds to clone 62 (1379bp). Clone 13 comprises 2104bp of the 3' region that were cut off the pUC18 vector by Sal1/Sst1 restriction, blunted with T4 DNA polymerase and ligated into the T4 DNA polymerase blunted BamHI site of pPZP121/35S, creating clone pPF13. The same procedure was followed for the 3' region of AtMSH6 clone 62 (1379bp) thus creating plasmid pPF14. For the double constructs, the 3' region (from clone 62) of AtMSH6 was introduced ahead of the AtMSH3 region into pPF13 creating pCW186 and reciprocally, the 3' region of AtMSH3 (from clone 13) was introduced ahead of AtMSH6 into pPF14, creating pCW187.

These constructs were introduced into the Arabidopsis cells (as described below) of wildtype Columbia and of the Columbia tester line.

An alternative strategy to antisense inhibition of AtMSH6 comes from experiments of 15 Marra et al. (1998. Proc. Natl. Acad. Sci USA 95. 8568-8573) who show that overexpression of functional MSH3 results in depletion of MSH6 protein in human cells. This depletion may generate a mismatch repair mutant phenotype.

For the purpose of overexpressing functional AtMSH3 protein in plant cells, the complete MSH3 coding region was excised from pPF26 (example 1) by digestion with 20 Smal, and was inserted into the Smal site of pCW164. The resulting construct was named pPF66. It contains a complete AtMSH3 gene under the control of the 35S promoter inside the left (LB) and right (RB) border of the T-DNA. This T-DNA also contains the hpt2 gene for gentamycin selection. Plasmid pPF66 was introduced into Arabidopsis cells as described below. One cell clone was selected which clearly overexpressed the AtMSH3 gene as shown by Northern analysis. Figures 12-16 provide plasmid maps of plasmids pPF13, pPF14, pCW186, pCW187 and pPF66, respectively.

Construction of tester construct

For the purpose of Forward Mutagenesis Assays, a tester construct was built containing the coding regions for nptII, codA, uidA. All three genes are driven by the 35S promoter and are terminated by the 35S terminator. This construct was obtained by introducing an EcoR1 fragment encoding the codA cassette (2.5kb) and a HindIII fragment encoding the uidA (GUS) cassette (2.4kb) into the pPZP111 vector (Hajdukiewicz et al.,1994, Plant Mol Biol 23: 793-799) which already contained the nptII expression cassette. This new plasmid was named pPF57. NptII is used to select for transformed plant cells.

35 GUS is used to analyse the degree of gene silencing in the construct (i.e. to identify cell lines in which the transgenes are expressed), and codA is used as a marker for forward mutagenesis (described below).

The plasmid map of pPF57 is provided in Figure 17.

Plant cell transformation

then transformed by co-cultivation. A suspension culture of Arabidopsis thaliana cells that 5 has been established by Axelos et al. (1992, Plant Physiol. Biochem. 30, 1-6) may be used. One day old freshly subcultured cells are diluted five times into AT medium (Gamborg B5 medium. 30g/l sucrose, 200µg/l NAA). 10µl of saturated Agrobacterium containing the transforming T-DNA constructs are added to 10ml diluted cells in a 100ml erlenmeyer. The co-cultivation is agitated slowly (80rpm) for 2 days. The cells are then washed 3 times into AT medium and finally resuspended in the same initial volume (10ml). The culture is agitated for 3 days to allow expression before plating on selection plates (AT/BactoAgar 8g/l+gentamycin 50µg/ml). Transformed individual calli are isolated 3 weeks later.

Tester Strain

The tester construct on plasmid pPF57 was introduced into Arabidopsis cells of wildtype Columbia using the transformation protocol described above. Among 10 candidate transformants, one cell clone was shown (by Southern analysis) to have a unique T-DNA insertion. All three genes were shown to be functional in this cell line as indicated by resistance to kanamycin, blue staining in the presence of X-Glu (GUS), and sensitivity to 5-fluoro-cytosine (codA).

MMR altering genes (described above) were then introduced individually into the tester line and transformed cells are used for analysis of both Microsatellite Instability and Forward Mutagenesis.

Microsatellite analysis

Microsatellites have been described in Arabidopsis (Bell and Ecker, 1994, Genomics 19, 137-144). The present Example is based on a study of instability of microsatellites that are polymorphic amongst different ecotypes. DNA is extracted from the transformed calli. Specific primers have been defined that are used to amplify the microsatellite sequence. One of the two primers is previously P³² labelled by T4 kinase. In case of a polymorphic variation, new PCR products appear that do not follow the expected pattern of migration on a polyacrylamide gel. This is a commonly observed feature for MMR deficient cells in yeast or mammalian cells.

In particular, the present Example describes a study on microsatellites ca72 (CA₁₈), nga172 (GA₂₉), and ATHGENEA(A₃₉), chosen because they belong to the types predominantly affected in human mismatch repair deficient tumors. The size of these microsatellites is not conserved from one *Arabidopsis* ecotype to the other.

Arabidopsis cells which are transformed with an MMR altering gene (above) and control cells not expressing the MMR altering gene are allowed to form calli. DNA is

rapidly extracted from the calli and is analysed for microsatellite instability as described in detail by Bell and Ecker 1994. Genomics 19, 137-144. In summary, the relevant microsatellite is amplified by PCR using P32 labelled primers. The PCR products are separated on a DNA sequencing gel for size determination. Size differences between microsatellites from transformed and control cells not expressing the MMR altering gene in question indicate microsatellite instability as a result of MMR alteration.

The sequences of primers used for PCR amplification of microsatellites ca72 and nga172 are included in Table 1. PCR amplification of microsatellite ATHGENEA made use of a forward primer containing the sequence

ACCATGCATAGCTTAAACTTCTTG (SEQ ID NO:32)

and of a reverse primer containing the sequence

ACATAACCACAAATAGGGGTGC (SEQ ID NO:33).

The amplification for microsatellite ca72 revealed in Columbia control cells (with respect to the MMR altering gene) a 248 bp long PCR fragment instead of the published length of 124 bp. DNA sequencing verified this fragment as a CA₁₈ microsatellite.

Forward mutagenesis assay

10

Tester cells transformed with antisense AtMSH3 or antisense AtMSH6 or both AtMSH3/AtMSH6 are analysed for the stability of the codA gene. The functional codA gene confers to sensitivity to 5-fluoro-cytosine (5FC), whereas a gene inactivating mutation in 20 codA will confer resistance to 5FC. The frequency of resistant cells is therefore a good indicator of somatic variation as a direct result of MMR alteration. Variants resistant to 5FC are first analysed for GUS activity. If GUS is inactive, 5FC resistance is assumed to be due to gene silencing (all three genes are under the 35S promoter). If GUS is active, 5FC resistance is assumed to be due to forward mutations that have inactivated codA. PCR is then performed on the putative codA mutant genes which is then sequenced to confirm the presence of forward mutations in codA.

Besides codA, other marker genes may also be used for the Forward Mutagenesis Assay such as the ALS gene (conferring sensitivity to valine or to sulfonylurea; Hervieu and Vaucheret, 1996, Mol. Gen. Genet. 251 220-224; Mazur et al. 1987, Plant Physiol. 85 1110-30 1117).

Example 3. Homeologous meiotic recombination in Arabidopsis thaliana

A. Construction of a meiocyte specific gene expression cassette comprising the DMC1 promoter and the NOS terminator

(i) The *DMC*1 promoter may be used as published by Klimyuk and Jones, 1997, 35 Plant J. 11.1-14). To obtain a more convenient alternative for gene cloning, a 3.3 Kb

long subfragment of the DMC1 promoter was obtained by PCR from genomic DNA of Arabidopsis thaliana (ssp. Landsberg erecta "Ler").

The PCR was done in three rounds:

Round One: A 3.7 Kb long product was obtained using the forward primer 5 DMCIN-A comprising the sequence

GAAGCGATATTGTTCGTG (SEQ ID NO:34)

and the reverse primer DMCIN-B comprising the sequence

AGATTGCGAGAACATTCC (SEQ ID NO:35).

The weak amplification product was then used as template for round two and three.

Round Two: A 3.1 Kb long product comprising the promoter and the 5' untranslated leader was obtained using forward primer DMCIN-1, which contained the sequence

acgcgtcgacTCAGCTATGAGATTACTCGTG (SEQ ID NO:36)

and introduced a SaII cloning site at the 5' end of the promoter fragment, and reverse primer DMCIN-2 which contained the sequence

gctctagaTTTCTCGCTCTAAGACTCTCT (SEQ ID NO:37)

and introduced a XbaI site at the 3' end of the PCR fragment.

Round Three: A 0.2 Kb long product comprising the first exon/intron of the DMC1 promoter was obtained using forward primer DMCIN-3, which contained the sequence

gctctagaGCTTCTCTTAAGTAAGTGATTGAT (SEQ ID NO:38)

and introduced a XbaI site at the 5' end of the PCR fragment, and reverse primer DMCIN-4, containing the sequence

teccegggetegagagatetecatggTTTCTTCAGCTCTATGAATCC (SEQ ID NO:39) and introduced at the 3' end of the PCR product restriction sites for Ncol, Bg/II. Xhol and 25 Smal.

The products obtained in round Two and Three were digested with XbaI and subsequently ligated to reconstitute a 3.3 Kb long DMC1 promoter from which the first two in-frame ATG start codons were replaced with a unique restriction site for XbaI. This promoter can be cloned between the restriction sites for SaII and SmaI of p3264, which contains the SacI-EcoRI NOS terminator in pBIN19, to yield the entire expression cassette in pBIN19. This cassette contains the following cloning sites: NcoI, BgIII, XhoI. SmaI and (already present on p3264) KpnI and SacI.

(ii) Another strategy yielded the following convenient *DMC*1 promoter. A 1.8 kb DNA fragment comprising the 3' terminal part of the meiocyte specific *DMC*1 promoter was isolated by PCR from purified genomic DNA of *Arabidopsis thaliana* (ssp. Landsberg erecta "Ler"). The forward PCR primer (DMC1a) contained the sequence

acgcgtcgacGAATTCGCAAGTGGGG (SEQ ID NO:40)

and introduced a Sall cloning site at the 5' end of the promoter fragment. The reverse PCR primer (DMC1b) contained the sequence

20

introducing a polylinker region at the 3' end of the promoter fragment. The PCR reaction was carried out with VENT DNA Polymerase (NEB) over 25 cycles using the following

cycling protocol: 1 minute at 94°C, 1 minute at 54°C, 2 minutes at 72°C.

The PCR reaction yielded a blunt ended DNA fragment which was digested with restriction enzyme SaII and was cloned into the cleavage sites of restriction enzymes SaII and SmaI in plasmid p2030, a pUC118 derivative containing the SacI-EcoRI NOS terminator fragment of pBIN121. The cloning yielded plasmid p2031, containing the DMC1 promoter-polylinker-NOS terminator expression cassette depicted in Figure 18.

10 B. Construction of an MSH3 antisense gene under the control of the DMC1 promoter

A 2.1 kb DNA fragment encoding the carboxyterminal part of AtMSH3 was removed from the polylinker of clone 13 described in Example 1 after (i) digestion with KpnI. (ii) blunting of the DNA ends generated by KpnI and (iii) digestion with BamHI. The isolated fragment was then cloned in antisense orientation downstream of the DMC1 promoter in plasmid p2031, which had been digested with restriction enzymes SmaI and Bg/II. This cloning yielded plasmid p2033 (Figure 18).

After digestion of p2033 with EcoRI, a 4.1 kb DNA fragment was recovered comprising the DMC1 promoter, the partial MSH3 cDNA in antisense orientation with respect to the promoter and the NOS terminator. This fragment was cloned into the EcoRI restriction site of plant transformation vector pNOS-Hyg-SCV to yield plasmid p3242 (Figure 18).

C. Construction of a combined MSH6/MSH3 antisense gene under the control of a single DMC1 promoter

A 3.1 kb fragment, encoding in antisense orientation the partial AtMSH6 and AtMSH3 sequences and the 35S terminator, was isolated from pCW186 by digestion with KpnI. The fragment was treated with Klenow enzyme to blunt both ends. It was then cloned into the SmaI site of plasmid p3243 (a pNOS-Hyg-SCV derivative, illustrated in Figure 19), which had been opened to delete the region between the SmaI sites. Clones containing the fragment in the antisense orientation with respect to the DMC1 promoter (described in A(ii) above) were identified by diagnostic digestion with BamHI. The selected construct was named p3261.

Another practical way of cloning the double antisense gene is as follows. A 1 kb DNA fragment encoding the carboxyterminal part of AtMSH6 is isolated from clone 62 described in Example 1 after digestion of clone 62 plasmid DNA with BamHI, which cleaves in the 5' polylinker region flanking the partial cDNA, and with EcoRI, which cleaves within the cDNA. The isolated fragment is treated with Klenow enzyme to blunt both its ends and is cloned into the recipient plasmid p2033 or p3242. For the purpose of

cloning, the recipient plasmid may be cleaved with either Aval or Ncol and can be blunted with Klenow enzyme to produce blunt acceptor ends for fragment cloning. This cloning yields two opposite orientations of cloned fragment DNA with respect to the DMC1 promoter. These can be identified by diagnostic digestion with restriction enzymes Scal or XmnI in conjunction with Sacl. The selected construct contains the DMC1 promoter, the combined partial cDNAs for AtMSH3 and AtMSH6 (both cloned in antisense orientation with respect to the DMC1 promoter) and the NOS terminator. If the recipient plasmid is p2033, the combined antisense gene under control the single DMC1 promoter is recovered from the vector after EcoRI digestion and is cloned into the EcoRI restriction site of pNOS-Hyg-SCV.

D. Construction of a full-length MSH3 sense gene under control of the DMC1 promoter for overexpression of functional MSH3 protein

Overexpression of MSH3 protein was shown in human cells (Marra et al., 1998, Proc. Natl. Acad. Sci. USA 95. 8568-8573) to complex all available MSH2 protein. This leaves MSH6 protein without its partner, leading to the degradation of MSH6 protein and eventually to a mismatch repair phenotype.

This phenomenon is exploited to increase homeologous meiotic recombination in Arabidopsis as an alternative to antisense inhibition of AtMSH6. For this purpose the full-length cDNA encoding AtMSH3 is isolated from plasmid pPF66 by digestion with Smal and is cloned into the Smal site of the DMC1 expression cassettes described in A(i).

E. Selection of Recombination markers on homeologous chromosomes of Arabidopsis thaliana subspecies Landsberg erecta (Ler), Columbia (Col) and C24, respectively

E(i). Visual recombination markers in Arabidopsis th. subspecies C24:

Agrobacterium mediated transformation with a T-DNA containing a 35S-GUS gene, inactivated by insertion of a 35S-Ac transposable element (Finnegan et al., 1993, Plant Mol. Biol. 22, 625-633), had yielded a C24 line in which the T-DNA construct was integrated into chromosome 2. Genetic and molecular analysis of this line shows that the Ac transposon had excised from its T-DNA locus thereby restoring GUS activity, but had re-inserted into the chromosome at a distance of 16.4 cM, where it stayed fixed (due to disablement of Ac) within the chlorina gene. Insertional inactivation of the chlorina gene caused a bleached phenotype in those plants that were homozygous for this mutation. Because of the two linked phenotypic markers, chlorina3A:Ac and GUS, this C24 line was used in crosses to wildtype Ler for analysis of meiotic homeologous recombination on chromosome 2 in conjunction with molecular recombination markers.

35 E(ii). Visual recombination markers in Arabidopsis th. Ler:

The Ler line NW1 (obtained from NASC, Nottingham, UK) contains one recessive visual marker per chromosome. i.e. an-1 on Chr.1, py-1 on Chr.2, gl1-1 on Chr.3, cer2-1

10

on Chr.4, and ms1-1 on Chr.5. This line is used in crosses to wildtype C24 which expresses an MMR altering gene for analysis of meiotic homeologous recombination on chromosomes 1-5 in conjunction with molecular recombination markers listed in Table 1.

Other Ler lines from NASC have several visual markers in close proximity to each other on the same chromosome. When these lines are used for hybrid production, analysis of homeologous meiotic recombination may make use entirely of visual recombination markers. Particularly suitable for crossing to C24 wildtype that is expressing a MMR altering gene are the following Ler lines:

NW22: relative markers are dis1 - (4 cM) - ga4 - (11 cM) - th1 on chromosome 1.

NW10: relevant markers are tz-201 - (5 cM) - cer3 on chromosome 5.

NW134, relevant markers are ttg - (4 cM) - ga3 on chromosome 5.

NW24 (abi3-1) and NW64 (gl1-1). When present in the same plant on chromosome 3. abi3-1 and gl1-1 are 13 cM apart. Since this marker combination is not available from NASC, we have combined these markers by crossing line NW24 to line NW64. The F1 offspring were allowed to self-fertilise and to produce F2 seeds. F2 Plants which carry both markers as homozygous traits on the same chromosome can be identified firstly, by germinating F2 seeds on germination medium containing selective concentrations of abscisic acid, and subsequently, by identifying among the abscisic acid resistant plants those individuals which show the glabra phenotype.

20 E(iii) Molecular recombination markers in Col, Ler and C24:

The genome of Arabidopsis thaliana is interspersed with unique base sequences arranged as simple tandem repeats. Allelic repeats can vary in length between different Arabidopsis subspecies and when amplified by PCR yield diagnostic DNA products of different length named Simple Sequence Length Polymorphisms (SSLPs). Many SSLPs have been genetically mapped and have been assigned to unique chromosome locations on the recombinant inbred map (Bell and Ecker, 1994, Genomics 19, 137-144; Lister and Deans lines, Weeds World 4i, May 1997).

In Table 1 are listed 28 mapped and established SSLPs between Ler and Col. A number of PCR primer pairs are described herein (SEQ ID NO:42 to SEQ ID NO:97) which also yielded SSLPs between C24 and Ler (19 SSLPs) or between C24 and Col (25 SSLPs), respectively. Polymorphic SSLPs can be used as molecular markers in the analysis of homeologous recombination between genomes from these subspecies.

The PCR reactions (25 μL) were carried out over 35 cycles (15 seconds at 94°C, 30 seconds at 55°C and 30 seconds at 72°C), with 0.25 U Taq DNA polymerase and 0.6 μg genomic DNA in reaction buffer containing 2 mM MgCl₂. PCR products were separated by agarose gel electrophoresis (4% ultra high resolution agarose) and visualised by ethidiumbromide staining. The results from the PCR experiments are summarised in

Table 1, which also shows the sequence of PCR primers, primer annealing temperature (Tm). PCR product length and chromosome location of SSLP (with respect to the RI map of May 1997, Weeds World 4i).

F. Production of hybrid plants

C24 plants heterozygous for chlorina3A:Ac/GUS are crossed as male to emasculated wildtype Ler to produce Ler/C24(chlorina3A, GUS) hybrid seeds.

Due to the heterozygosity of the C24 parent, only 50 % of hybrid plants have inherited the chlorina3A:Ac/GUS locus. The remaining 50% of hybrid plants are wildtype with respect to chlorina3A:Ac/GUS. Since the mutant locus is linked to a kanamycin resistance gene (contained on the same T-DNA as GUS) mutant plants can be pre-selected by germinating hybrid seeds on germination medium containing 50 mg/L kanamycin.

Ler plants homozygous for the five chromosome markers are male sterile (ms1-1) and are crossed without emasculation to wildtype C24 to produce Ler(an-1, pv-1, gl1-1, cer2-1, ms1-1)/C24 hybrid seeds.

Other Ler plants, which are male fertile, are crossed after emasculation of the female parent to produce Ler/C24 hybrid seeds.

G. Introduction of MSH3 and MSH6/3 antisense genes into Arabidopsis and analysis of meiotic homeologous recombination

(i) Transformation of hybrid plants and analysis of homeologous meiotic recombination

The plant transformation vectors comprising the antisense genes described in (B) and (C) above are introduced into Agrobacterium tumefaciens strain AGL1 (Lazo et al., 1991, Bio/Technology 9, 963-967) by electroporation. Recombinant Agrobacterium clones are selected on LB medium containing 50 mg/L rifampicin and 100 mg/L carbenicillin. Selected clones are used to infect roots of Arabidopsis hybrid plants (described in (F) above) using the root transformation protocol of Valvekens et al. (1988, PNAS 85, 5536-5540) except that shoot and root inducing media contain hygromycin (10 mg/L) instead of kanamycin.

Plants regenerated from roots of hybrid plants are genetic clones of root donating plants and therefore are again genetic hybrids of two Arabidopsis subspecies described in 30 (F). However, in contrast to the root donating plants, the regenerated hybrid plants also contain the introduced transgene and the co-introduced hygromycin resistance gene with the latter allowing these plants to grow on hygromycin containing culture medium.

Hygromycin resistant plants are then allowed to enter the reproductive phase and to produce gametes by meiotic divisions of microspore and megaspore mothercells. At meiosis, the *DMC*1 promoter is activated and can direct the expression of antisense genes described in (B) and (C) above, leading to decreased *MSH*6 and/or *MSH*3 gene

expression. This in turn depletes the gamete mothercells of MSH6 and/or MSH3 protein, thus causing alteration of MMR during meiotic divisions and increasing the recombination frequency between homeologous chromosomes.

Transgenic plants are then allowed to self-fertilise and to produce seeds. These 5 seeds (F2 seeds with respect to hybrid production), and the plants derived therefrom, carry the homeologous recombination events which can be identified by using the visual and molecular recombination markers described in (E) above.

In case of homeologous recombination between chromosomes of Ler and C24(chlorina3A:Ac. GUS), the analysis concentrates on chromosome 2 by selecting plants showing the visual phenotypic marker chlorina. This marker thus serves as a reference point as it indicates that respective chromosomes 2 originate from C24. Other markers, such as GUS or molecular markers, on chromosome 2 may then be used to identify chromosomal regions which are derived from the Ler chromosome as a result of homeologous recombination. F2 plants of control transformants not expressing the antisense gene(s) can be analysed in parallel and the results can be used for comparison to homeologous recombination results obtained in antisense plants.

(ii) <u>Transformation of C24 wildtype</u>, hybrid plant production and analysis of homeologous meiotic recombination

Introduction of MMR altering genes into wildtype C24 is done using the root transformation protocol as described in G(i) for transformation of hybrid plants. Transformed plants are selected by resistance to either 10 mg/L hygromycin (in case of transformation with T-DNA's derived from pNOS-Hyg-SCV) or to 50 mg/L kanamycin (in case of transformation with T-DNA's derived from pBIN19).

Transgenic plants are then allowed to self-fertilise and to produce seeds (T1 seeds).

25 Segregation of the antibiotic resistance gene in the T1 population then indicates the number of transgene loci. Lines with a single transgene locus (indicated by a 3:1 ratio of resistant:sensitive plants) are selected and are bred to homozygosity. This is done by collecting selfed seeds (T2) from T1 plants and subsequent testing of at least four independent T2 seed populations for segregation of the antibiotic resistance gene. T2 populations which do not segregate the antibiotic resistance gene are assumed to be homozygous for both the resistance gene and the linked MMR altering gene.

C24 plants homozygous for the MMR altering gene are then crossed to Ler lines homozygous for recessive visual markers (see E(ii)) to produce C24/Ler hybrid plants as described in (F). These F1 hybrids are then allowed to enter the reproductive phase and to produce gametes by meiotic division of microspore and megaspore mothercells. At meiosis, the DMC 1 promoter is activated and can direct the expression of antisense or sense genes described in (B), (C) and (D) above, leading to decreased MSH6 and/or MSH3 gene expression. This in turn depletes the gamete mothercells of MSH6 and/or MSH3

protein, thus causing alteration of MMR during meiotic divisions and increasing the recombination frequency between the homeologous chromosomes of C24 and Ler. Recombination events are then scored in the F2 generation.

For recombination analysis, the hybrid plants are allowed to self-fertilise and to produce F2 seeds. F2 plants are then preselected for a first visual marker. Since this marker is recessive, its visual presence indicates homozygosity for Ler DNA at the relevant locus. Those F2 plants which show this first visual marker are then analysed for the presence or absence of a second visual marker which in the Ler parent is closely linked to the first marker. Absence of the second visual marker indicates recombination between the relevant C24 and Ler chromosomes between the first and second marker. The frequency of recombination in transgenic hybrids is compared to the recombination frequency in control hybrids not expressing the MMR altering gene.

Examples of recombination analysis are the following.

The Ler line NW22(dis1, ga4, th1) is used for crosses to transformedC24.

F2 plants are preselected first for thiamine requirement (th1) and then are further analysed for re-appearance of wildtype height (loss of ga4) and/or re-appearance of normal trichomes (loss of dis1) as a result of recombination.

The Ler line NW10(1z-201, cer3) is used for crosses to transformed C24.

F2 plants are then preselected first for thiazole requirement (tz) and then are further 20 analysed for re-appearance of normal. i.e. non-shiny stems (loss of cer3) as a result of recombination.

The Ler line NW134 (ttg, ga3) is used for crosses to transformed C24. F2 plants are first preselected for dwarfish appearance (ga3) and are then analysed for re-appearance of trichomes (loss of ttg) as a result of recombination.

Ler plants homozygous for abi3-1 and gl1-1 are used for crosses to transformed C24. F2 plants are first preselected for their ability to germinate in the presence of abscisic acid and are then analysed for re-appearance of trichomes on the leaves (loss of gl1-1) as a result of recombination.

In the case of homeologous recombination between transformed C24 and the Ler line 30 NW1 (an-1, py-1, gll-1, cer2-1, msl-1), recombination analysis is similar the one described above, except that the second marker is not a visual marker but has to be a molecular marker. This is because the Ler parent carries only one visual marker per chromosome.

	L	TABLE 1: SS	SSLP Markers in Arabidopsis thaliana Subspecies	naliana S	ubspecies		
Chromosome	RI Map Position	PCR Primer Pair	Primer Sequence	Tm (°C)	length/COL	length/LER	length/C24
	2.3	ATEAT! F	GCCACTGCGTGAATGATATG	57.8	172	162	162
		ATEAT! R	CGAACAGCCAACATTAATTCCC	58.2			
_	9.3	NGA63 F	AACCAAGGCACAGAAGCG	57.3	=	68	120
		NGA63 R	ACCCAAGTGATCGCCACC	59.6			-
-	40.1	NGA248 F	TACCGAACCAAAACACAAAGG	56.1	143	129	no amplific.
		NGA248 R	TCTGTATCTCGGTGAATTCTCC	58.2			
-	81.2	NGA128 F	GGTCTGTTGATGTCGTAAGTCG	60.1	180	<u>8</u>	no amplific.
		NGA128 R	ATCTTGAAACCTTTAGGGAGGG	58.2			
_	81.2	NGA280 F	CTGATCTCACGGACAATAGTGC	1.09	105	85	85
		NGA280 R	GGCTCCATAAAAGTGCACC	57.8			
_	111.4	NGAIII F	CTCCAGTTGGAAGCTAAAGGG	99	128	162	170
		NGAIII R	TGTTTTTAGGACAAATGGCG	70			
=	ca. 7.5	NGA 168 F	CCTTCACATCCAAAACCCAC	57.8	213	217	208
		NGA 168 R	GCACATACCCACAACCAGAA	57.8			

,							
	70	NCA11261	CGCTACGCTTTCGGTAAAG	87.8	161	661	961
	Çğ. 49	NGA1126R	GCACAGTCCAAGTCACAACC	6.65			
		117047014	AAAGAGATGAGAATTTGGAC	51.7	114	120	114
.=	62.2	NUASOIL	ACATATCAATATATAAAGTAGC	49.5			
		NGASOIK	ACALAICAGUA		-		
				7 03	151	135	135
	73	NGA168 F	TCGTCTACTGCACTGCCG	07.0	101	3	
		NGA168 R	GAGGACATGTATAGGAGCCTCG	6.19			
	22	AibBIO2 I	TGACCTCCTCTTCCATGGAG	59.9	141	209	139
=	Ca. //	2 201017	TTAACAGAAACCCAAAGCTTTC	54.5			
		Ambiot n					
			A S C C A A A T G T C C A T T T C A T T G	54.1	146	148	148
=	ca. 83	Ain Ubique L		57.8			
		AthUBIQUE R	ACGACATOGCAGATITICA				
							9
	7.6	NGA172 F	AGCTGCTTCCTTATAGCGTCC	09	162	136	140
		NGA172 R	CATCCGAATGCCATTGTTC	55.4			
	9	NCA126 E	GAAAAACGCTACTTTCGTGG	56.1	119	147	no amplific.
	17.8	. .	CAAGGGATATCAAGAGCAGC	58.2			
		NUAI20 N		-			
				0 3	601	80	no amplific.
Ξ	17.5	NGA162 F	CATGCAATTTGCATCTGAGG	33.8	/21		
	·	NGA162 R	CTCTGTCACTCTTTCCTCTGG	- 1			

=	8.1.8	NGA6 F	TGGATTTCCTCCTCTTCAC	56.1	143	123	143
		NGA6 R	ATGGAGAGCTTACACTGATC	56.1			
٨١	8.61	NGA12 F	AATGTTGTCCTCCCTCCTC	59.9	247	234	220
		NGA12 R	TGATGCTCTCTGAAACAAGAGC	58.2			
			- ,				
λl	24.1	NGA8 F	GAGGCCAAATCTTTATTTCGG	56.1	154	861	961
		NGA8 R	TGGCTTTCGTTTATAAACATCC	54.5			
<u>\</u>	102	NGA1107 L	GCGAAAAACAAAAAATCCA	50.2	150	140	140
		NGA1107 R	CGACGAATCGACAGAATTAGG	58			
>	8.11	NGA225 F	GAAATCCAAATCCCAGAGAGG	58	611	189	611
		NGA225 R	TCTCCCCACTAGTTTTGTGTCC	1.09			
>	16.7	NGA249 F	TACCGTCAATTTCATCGCC	55.4	125	115	115
		NGA249 R	GGATCCCTAACTGTAAAATCCC	58.2	-		
>	6.61	CA72 F	AATCCCAGTAACCAACACACA	56.3	124	110	110
		CA72 R	CCCAGTCTAACCACGACCAC	61.9			
>	20	NGA151 F	GTTTTGGGAAG1TTTGCTGG	55.8	150	120	130
	·	NGA151 R	CAGTCTAAAAGCGAGAGTATGATG	58.6			
				-			

		:	ij ja	1 09	157	123	130
>	24	NGA106 F	CITALCCACITICIACCCAC				
		NGA 106 R	TGCCCATTTGTTCTTCTC	55.8			
	-				,	111	113
	37 B	NGA139 F	AGAGCTACCAGATCCGATGG	59.9	1/4	132	75.
>	37.0	NGA130 B	GGTTTCGTTTCACTATCCAGG	55.8			
		W CONON					
	5	NCA76 F	GGAGAAATGTCACTCTCCACC	3.	231	> 250	300
>	20	a graph	COCCACACACATTACG	57.8			
		NGA76 K	AGGCATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				
		10.00	CTCCACCAATCATGCAAATG	55.8	148	156	146
>_	61.1	ATHSOIN L					
		ATHSO191 R	TGATGTTGATGGAGATGGTCA	53.7			
					177	179	172
>	81.7	NGA129 F	TCAGGAGGAACTAAAGTGAGG	00.1	-		
		NGA129 R	CACACTGAAGATGGTCTTGAGG	60.1			

CLAIMS

- 1. An isolated and purified DNA molecule comprising a polynucleotide sequence encoding a polypeptide functionally involved in the DNA mismatch repair system of a plant.
- 2. A DNA molecule according to claim 1 wherein said polypeptide is homologous to a mismatch repair polypeptide of a yeast or of a human.
 - 3. A DNA molecule according to claim 1 wherein said polypeptide is homologous to AtMSH3 (SEQ ID NO: 19) or to AtMSH6 (SEQ ID NO: 31).
- 4. An isolated and purified polypeptide functionally involved in the DNA 10 mismatch repair system of a plant.
 - 5. A polypeptide according to claim 4 which is homologous to a mismatch repair polypeptide of a yeast or of a human.
- 6. An isolated and purified polypeptide selected from the group consisting of a polypeptide encoded by the gene AtMSH3 (SEQ ID NO: 18), a polypeptide encoded by the gene AtMSH6 (SEQ ID NO:30), polypeptides homologous to a polypeptide encoded by the gene AtMSH3 (SEQ ID NO: 18) and polypeptides homologous to a polypeptide encoded by the gene AtMSH6 (SEQ ID NO:30).
- 7. An isolated and purified DNA molecule comprising a polynucleotide sequence selected from the group consisting of (i) a sequence encoding a polynucleotide which is capable of interfering with the expression of a plant polynucleotide sequence encoding a polypeptide which is homologous to a mismatch repair polypeptide of a yeast or of a human and thereby disabling said plant polynucleotide sequence; and (ii) a sequence encoding a polypeptide capable of disrupting the DNA mismatch repair system of a plant.
- 8. A DNA molecule according to claim 7 comprising a polynucleotide sequence encoding a polynucleotide capable of interfering with the expression of a plant polynucleotide sequence encoding a polypeptide which is homologous to a mismatch repair polypeptide of a yeast or of a human and thereby disabling said plant polynucleotide sequence.
- 9. A DNA molecule according to claim 8 wherein said polynucleotide is capable 30 of interfering with the expression of a plant polynucleotide sequence is a sense polynucleotide, an antisense polynucleotide or a ribozyme.
 - 10. A DNA molecule according to claim 7 comprising a polynucleotide sequence encoding a polypeptide capable of disrupting the DNA mismatch repair system of a plant.

- 11. A DNA molecule according to claim 10 wherein said polypeptide is homologous to AtMSH3 (SEQ ID NO: 19) or to AtMSH6 (SEQ ID NO: 31).
- 12. A DNA molecule according to claim 10 further comprising a regulation element capable of causing overexpression of said polypeptide in a cell of said plant.
- 5 13. A chimeric gene comprising:
- a DNA sequence selected from the group consisting of (i) a sequence encoding a polynucleotide capable of interfering with the expression of a plant polynucleotide sequence encoding a polypeptide which is homologous to a mismatch repair polypeptide of a yeast or of a human and thereby disabling said plant polynucleotide sequence, and (ii) a sequence encoding a polypeptide capable of disrupting the DNA mismatch repair system of a plant; and

at least one regulation element capable of functioning in a plant cell.

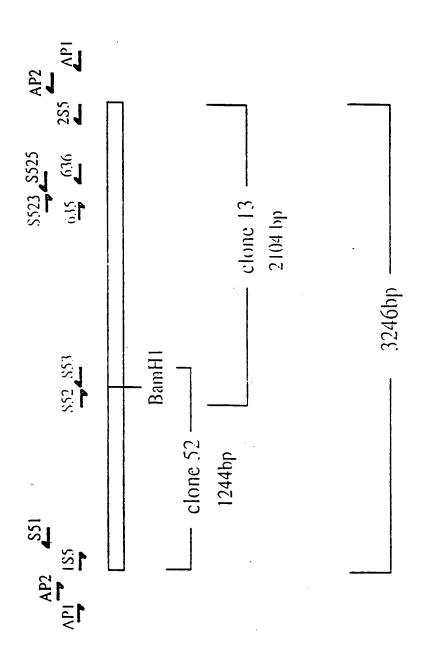
- 14. A chimeric gene according to claim 13 wherein said regulation element is selected from constitutive, inducible, tissue type specific and cell type specific promoters.
- 15. A chimeric gene according to claim 13 comprising a DNA sequence encoding a polypeptide capable of disrupting the DNA mismatch repair system of a plant, wherein said regulation element is capable of causing overexpression of said polypeptide in a cell of said plant.
- 16. A chimeric gene according to claim 13 wherein said regulation element is selected from the group consisting of 35S, NOS, PR1a, AoPR1 and DMC1.
 - 17. A plasmid or vector comprising a chimeric gene according to any one of claims 13-16.
 - 18. A plant cell stably transformed, transfected or electroporated with a plasmid or vector according to claim 17.
- 25 19. A plant comprising a cell according to claim 18.
 - 20. A plant according to claim 19 selected from plants of the families Brassicaceae, Poaceae, Solanaceae, Asteraceae, Malvaceae, Fabaceae, Linaceae, Canabinaceae, Dauaceae and Cucurbitaceae.
- 21. A process for at least partially inactivating a DNA mismatch repair system of a plant cell, comprising transforming or transfecting said plant cell with a DNA molecule according to any one of claims 1-3 or 7-12 and causing said DNA sequence to express said polynucleotide or said polypeptide.
 - 22. A process for at least partially inactivating a DNA mismatch repair system of a plant cell, comprising transforming or transfecting said plant cell with a chimeric gene

according to any one of claims 13-16 and causing said DNA sequence to express said polynucleotide or said polypeptide.

- 23. A process for at least partially inactivating a DNA mismatch repair system of a plant cell, comprising transforming or transfecting said plant cell with a plasmid or vector according to claim 17 and causing said DNA sequence to express said polynucleotide or said polypeptide.
- 24. A process for increasing genetic variation in a plant comprising obtaining a hybrid plant from a first plant and a second plant, or cells thereof, said first and second plants being genetically different; altering the mismatch repair system in said hybrid plant; permitting said hybrid plant to self-fertilise and produce offspring plants; and screening said offspring plants for plants in which homeologous recombination has occurred.
- 25. A process according to claim 24 wherein a first gene is incapacitated in said first plant, a second gene is incapacitated in said second plant, and said first and second genes are incapacitated in said hybrid plant thereby altering the mismatch repair system of said hybrid plant.
 - 25. A process according to claim 25 wherein said incapacitation of the mismatch repair system of said hybrid plant is reversible.
- 26. A process according to claim 24 wherein a new genetic linkage of a desired characteristic trait or of a gene which contributes to a desired characteristic trait is 20 observable in at least one of said offspring plants.
- 27. A process for obtaining a plant having a desired characteristic, comprising altering the mismatch repair system in a plant, cell or plurality of cells of a plant which does not have said desired characteristic, permitting mutations to persist in said cells to produce mutated plant cells, deriving plants from said mutated plant cells, and screening said plants for a plant having said desired characteristic.
- 28. A process according to claim 27 wherein said step of altering the mismatch repair system comprises introducing into said hybrid plant, plant, cell or cells a chimeric gene according to claim 13 and permitting the chimeric gene to express a polynucleotide which is capable of interfering with the expression of a plant polynucleotide sequence in a mismatch repair gene of the hybrid plant, plant, cell or cells, or a polypeptide capable of disrupting the DNA mismatch repair system of the hybrid plant, cell or cells.
 - 29. A process according to claim 28 comprising inactivating an MSH3 gene and/or an MSH6 gene of said plant.
- 30. A process according to claim 28 comprising inactivating an MSH3 gene and an MSH6 gene of said plant.

- 31. A process according to claim 27 comprising at least partially inactivating the mismatch repair system of said plant in a predetermined cell type or in a predetermined tissue of said plant.
- 32. A process according to claim 31 further comprising restoring mismatch repair 5 in said cell type or said tissue.
 - 33. An oligonucleotide capable of hybridising at 45°C under standard PCR conditions to a DNA molecule according to claim 1 with the proviso that said oligonucleotide is other than SEQ ID NO:1 or SEQ ID NO:2.
- 34. An oligonucleotide capable of hybridising at 45°C under standard PCR to conditions to the DNA of SEQ ID NO: 18 with the proviso that said oligonucleotide is other than SEQ ID NO:1 or SEQ ID NO:2.
 - 35. An oligonucleotide capable of hybridising at 45°C under standard PCR conditions to the DNA of SEQ ID NO:30 with the proviso that said oligonucleotide is other than SEQ ID NO:1 or SEQ ID NO:2.

Figure 1



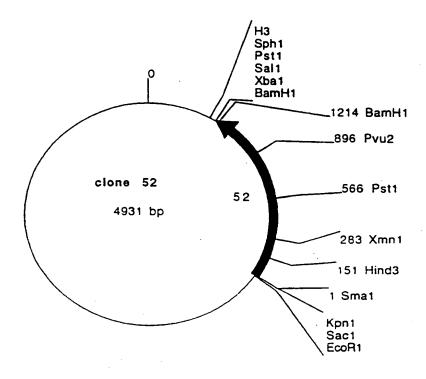


Figure 2

Comments/References: 52= 3' side of S5 (AtMSH3) 1244bp in pUC18/Sma1

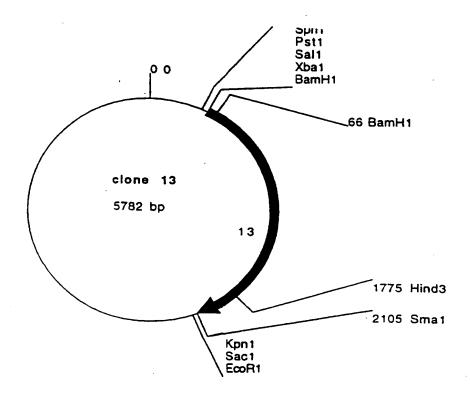


Figure 3

Comments/References: 13 = 3' side of S5 (AtMSH3) 2104bp in pUC18/Sma1

प	
Φ	
H	
2	
ס	
ᇤ	

80	144 15	204 35	264 55	324 75	384 95	444 115	504 135	564 155	624 175	684 195	744	804 235	864 255	924 275
agcgcgcgaaaa ttggcaacccaagttcgccatagccacgaccacgacctt ccatttctcttaaacggagga	CCC	CCG P	CTC L	GAT D	GTT V	AAG K	GGA G	TTC	GCA A	GCA A	GAA E	AAT N	GAA E	GTT V
ACGG	GCT A	CCA P	CAC H	000 6	TAT Y	CTA L	TTC	N N	AAT N	GGT G	CTT L	AGT S	ATT I	GTT V
TTAA	TTC	CCG P	GAC D	GTA V	GAA	GAG E	TTC F	CAC H	GTG V	CAT H	ACG T	CAG Q	GGT G	GAA E
TCTC	TTC	ACA T	TCC	CCA P	GAG E	GTG V	AGA R	GAT D	CTG L	TCC	GCC A	TCA S	TGT C	GGT
CATT	CGT R		CTC	AAC N	CCG P	GTG V	TAC Y	ATG M	AGA R	AAG K	A AAA	GGT G	၁၁၁	ACA T
CTTC	TCT	TCA	CTT L	CAA	TCG S	CAA	AGG R	CAT H	AGA R	ATT I	ACC T	TTT F	TTA L	TCG S
CGAC	ATT I	GAA E	AAG K	ACT T	000 000	CAG Q	TAC Y	GCT A	GTG V	GCC A	TAT Y	GG'I G	ACA T	ATT
ACCA	ACG T	200	CGT R	CAC H	GAA E	G E	GGT G	TAC Y	CAT H	GCA A	TTG L	GAA E	GAG E	GAA E
CACG	CAG	GT'A V	AAG K	CCT P	CTG L	TTG L	GTT V	AT'F I	TTC F	ACT T	GCG A	GAA E	TCG	GTT V
TAGC	CAG Q	CCG P	TCC S	TCT S	TTT F	CCA P	GAA E	GGT G	AAT N	GAA E	TCG S	GGT G	A.A.G K	၁၅၅
GCCA	A.A.G K	AAT N	CCT	CTT L	AGA R	ACA T	GTG V	TTG L	TTG L	ACT T	CTG L	GGT G	GTT V	GTT
GTTC	CAA	CCG P	TCT S	AAA K	CAG O	TAC Y	ATG M	GTG V	CGA R	CAG	GCA G	TGT	AGA R	GTT V
CCAA	A.A.G	GAA E	TTC	CCT	CTC L	A.A.A K	TTG L	CGC R	TTT F	AAG K	CGG R	GGT G	GAG E	GGT G
CAAC	ວງງ	CAC	TCC	AAG K	TTT F	AGG R	GTT V	GCA A	ACA	GTG V	TTC F	GGT G	GAT D	GTC V
TTGG	ATG M	ACT T	GTA V	AAA K	AGA R	TCG S	GTG V	GCA A	CCA P	GTA V	TTT F	AGT S	GTG V	AGA R
AAAA	ATAAAGCAATT	CCG P	ACT	CCC	CAA	TCA		ATC I	GTG V	GGT G	CCT P	ATA I	GTT V	GTT
ອວອວ	AGCA	TCC S	9 8 8	TCA S	CAC H	TCA	CCA P	GAG	AGT S	ATT I	၁၁၁	GAT D	TGT C	GAT D
AGCG	ATAA	X &	TCC S	GCG A	TTA L	ACG T	TAC Y	GCG A	GCG A	A.A.G K	ACC T	GAG E	GTT V	rrt F
	ACGA	ည မ	ATA I	22 9	AAT	GA.	AAG K	GAC	ACG T	TAC Y	ივი ო	GCT A	TTG L	AGT S
CTAAGAA	GATTACG/	A A A	AAG K	225 4	, 200 a	000 6	AGC S	GAA E	ATG M	GGA G	AAC	GCG A	T'IC F	ATG M
~	81 1	145 16	205 36	265 56	325 76	385 96	445 116	505 136	565 156	625 176	665 196	745 216	805 236	865 256

1884 595	1944 615	2004 635	2064 655	2124 675	2184 695	2244 715	2304 735	2364 755	2424	2484 795	2544 815	2604 835	2664 855	2724 875
ATT TCA I S	GCG GCT A A	CTT GCT L A	TCA TTT S F	CAT TTG H L	ACC AAG T K	CTA GCA L A	TTC AGT F S	TTG CAC L H	GAC TGT D C	TTA CAA L Q	ATT ATC I I	TCC ATA S I	GAT GGT D G	CTA GAA L E
GTT A7 V I	GAA G(GAG C' E L	GCT T	ACA C T H	AGC A S T	GCT C	AGT T S F	TGT T C I	GAT C	ATA 1 I	CAA 7	ATT I	CTT (TTT
rcr G' s v	AAG G K E	CCT G	ATA G I A	ATC A I T	AAT A N S	CTA G	AAG P	GAC 1 D (GTG (ACT /	16C (TTA L	GTG V	ACC T
•	AAT AA N K	TTT C(F P	TCG A'S	GGG A'	GTA A V	GAG C E L	CTC A	CTG G	TTT G	GAG P	TAT 1 Y	GCT 1	CAC (AGT 1
G ATT I				TCG G(S G	MAA G. K	GAT' G	TTC C	GCA C	GAG TE	CTG G	GAA T	GTT G	CTG C	AGA PR
A TTG L	c CTA	c cAA	T TCC S			TTG 67	AGT TY S F	GCT G	CCC G	GTA C	3 55 5 G E	CAA G	AAG C K	GGC A G R inu c
. K	, GCC	GAC D	GAT D	4 GTG	s GTG V								GCC A	CAT G H G onti
AGA R	TCT	AGC S	CTG L	CAA	TGG W	550	GAT D	r CTT L	CCT R	r cct P	A GAA	c ccT		7 \
TTG L	CTC L	TCC S	AAG K	CTT L	A.A.T N	CCT A	TGG W	GCT A	GTC V	CAT H	GCA	ATC I	TTC F	CAG
CTT L	CTT L	ACT T	GAA E	TTT F	ATG H	GTA V	TCG S	CAA	TAT Y	CGT R	CAT H	TAT Y	S	ATC I
ACT	A.A.A.	A'I'C I	AGG R	GA.A E	CCT P	A'f'A I	GCT A	GTT V	AAC	GGT	TTG L	76C C	900 A	AGT A S I
rcr /	GGA G	CTA	ATC I	TTG L	GTC V	GAA E	CGA R	ر ودد	AAG K	TCT S	ATT I	AGC S	CCA P	GAC D
CGA R	229	ATA	GTC V	AAT	AAG K	CCA	AAC	GCT A	AAC	cAG Q	ACA T	AAG K	GTA V	TCA
GTG (AAT	GAC , D	TTA I.	CGA R	TCC S	၁၁၁ ၂	GTG V	AAG K	AGA R	ATA I	GAC D	GGA G	TTT E	GCT A
ACT (GAC 7	CTC (GTT V	ATT	GAT D	CAT H	ATT I	TTT F	TCT	N AAC	AAT N	GGA G	TCC S	GGT
GCA A	GTT (TTG	GCA	GCT	GTT V	TAT Y	gcc A	GAT D	CTA L	ATA I	CCA P	ATG M	GGT G	ATG
TCT (GTG (GAC 7	CAA	CTC)) 	CGA R	CTT	ACA T	ACT	GAG E	GTC V	A AC	GTT V	იც გ
CAA O		66T (AAG K	CTG L	ATT	CAT H	TAC Y	TCA	GTT V	TTC F	CCT	CAG Q	ACT T
ATG O			GCT (AAG 1	GAG (ACT	GAA	TAC Y	CTT	A.	AAC	GGA	GCT A	TTC
AGT A S M				CGC P	ATA (AAG 1	ACT (AGA .					ATG M	GTT
1825						2185 696	2245	2305	2365 756	2425	2485	2545 816	2605	2665 856

2784 895	2844 915	2904 935	2964 955	3024 975	3084 995	3144	3204 1035	3264 1055	3324 1075	3397 1082	3458 5	3522 16
TTA L	TTA L	ATA I	ACA T	GTG V	CCA P	AGA R	GAA	GAC	CTA	TGA TTTAATCTTAACATTATAGCAACTGCAAGGTCTTGATCATCTGTTAGTTGCG	500 6	
ATA I	ACA T	GAA E	CTG L	CTT L	CCT P	GCA A	GAA E	GAG E	AGA R	rtag	AAT N	AA.
GTT V	GCA A	CCT P	TAT Y	AAG K	ATA I	CGT R	GCA A	GAA E	ATC I	cre	TCT /	AAA
CTT L	TAT Y	TAC Y	TCG	TAT Y	CAG Q	GTA V	၁ဗ္ဗ	TCT S	X X	VTCAT	GAT 1	AAAA
TCG S	9 8 8	CAT H	GTC V	CTA L	GCC A	GAG E	AGA R	CTC L	ეეე ეეეე	TTG	ATG (AAAA
CGT R	ATT I	ACG T	CAT H	TAC Y	CTT L	GCT A	000 P	GCT A	GCT	AGGTC	TAG AGAG A	TAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
TCT S	gcc A	GTC V	TAC Y	ACC T	CAG Q	GAA E	GAA E	T'IT F	ATT 1	rgca)G A(JAAA inu
TCT S	GTA V	TTT F	ACA T	GTG V	GCT A	TTG L	GAA E	§×	AAG K	AAC	MT TW	qaaaaaaaaaaa (Continued)
TGT	GGT	CTT L	ეეე ეეე	GAT D	GTT V	AAA K	CAT H	CTG L	TGG W	TAG	GAG N	AAA CO
ACC T	GAC	GTT V	GTT V	GAT D	AAG K	GCA A	GGA G	GAC	GCT A	CATT	AAA G	GCA TAA AA A Figure 4
AGA R	CAC H	TTG L	TCT	CAT H	TTT F	GCT A	GAA E	GCA A	CA1	TTAAC	A X	GCA A igu
ATC I	ACA T	TGT C	GGT	GAT D	GGT	ATG M	CCA P	TTT F	AAG K	MTCI	ACA AGA I	ညည် ရ
ATA I	AGC S	AGA R	CCA	TAT Y	TTT	TCA S	GAA E	TTG L	TTA L	TTT	ATA AC I	CCA P
CAC H	ACT T	A.A.G K	TTC F	AGT S	AGC S	ATT I	GGA G	GAC D	TTT E	TGA.	AGT AT S I	rcr s
TCA S	၁၅၅	GAA E	GGA	၁၅ ၁	AGG R	225 8	ATG M	GGT	GAG E	TTT F	ATT AC	TTT
GCG A	AGA R	GCA A	AAC N	A A	AGC S	CGA R	CGC R	C'I'A L	TTC F	TCA	TGT A7 C I	ATC
GAA	SGA G	CTA L	AGT S	GAT	76C C	CGT R	ACA T	GCT A	GCA A	TGT C	ATG TC	TAC
AGT S	CTT L	CTC L	ATC I	A AG	CTT L	ATA I	AAT	TCG S	A A	ACT T		CAG O
TTA L	GAG E	CAT H	GAG E	CAG	GGT	TGT C	AGA R	ATT I	TGG W	CCA P	TACTAACTT	TTG L
GAA E	GAT D	CAG O	GCT	TTG L	CGT R	TCA	GAG	TCT	CCT P	A.A.A	TACI	GTG V
2725 876	785	1845 916	2905 936	965 956	1025 976	966 996	1145	3205 1036	3265 1056	3325 1076	3398 1	3459 6

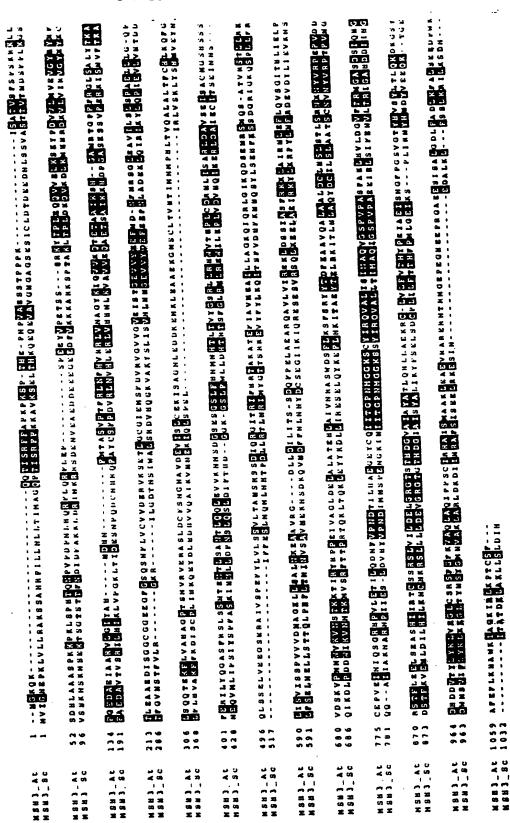
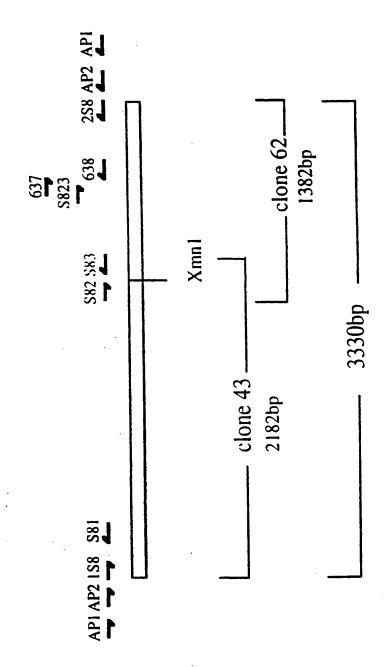


Figure 6



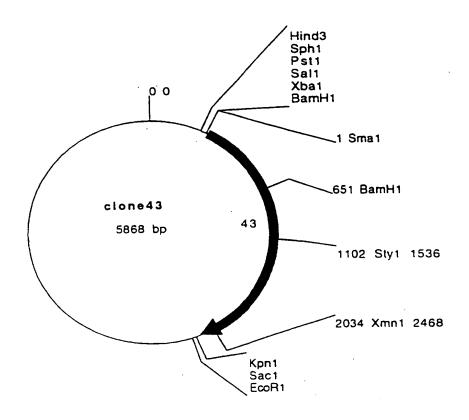


Figure 7

Comments/References: 43= 5' side of S8 (AtMSH6) 2182 bp in pUC18/Sma1

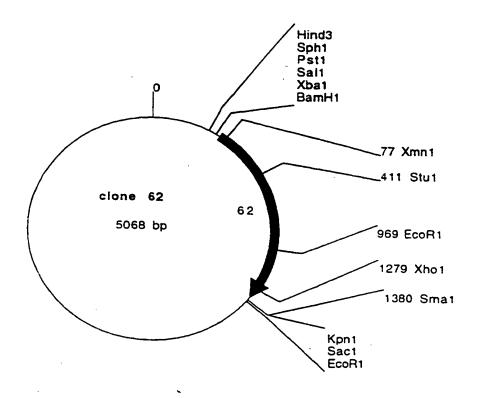


Figure 8

Comments/References: 62= 3' side of S8 (AtMSH6) 1379bp in pUC18/Sma1

•	
a)	
ŭ	
7	
F	
۳.	
77.	
igure	

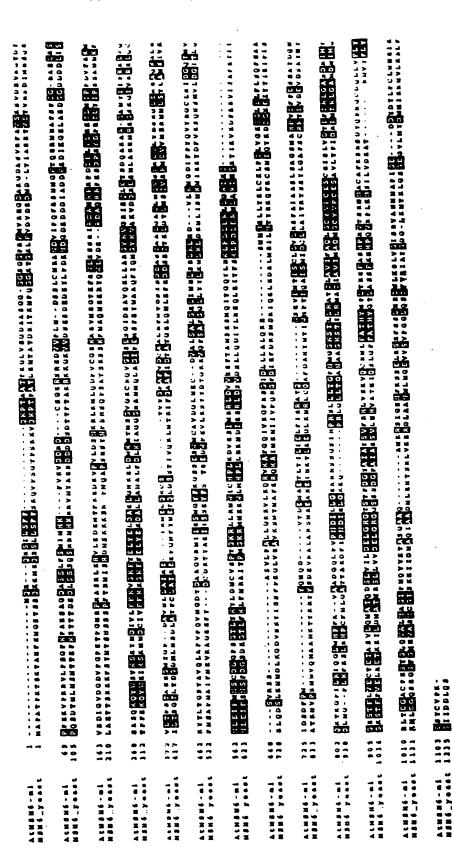
80	. 153	213 24	273	333 64	393 84	453 104	513 124	573 144	633 164	693 184	753	813 224	873 244	933 264
သသ	(1)	TCC	999 999	AGA R	CCG P	AAA. K	GAT D	X K	GAA	GCT A	GTA V	GAA E	AGA R	TTC F
rrcc	CAG	GTT ?	GAA (GTT V	AAG K	GTA V	AAT N	GGT G	GTA V	CGT R	CCT P	K AA	AAT N	GTT V
rcti	s cgc R	TTG (AAG (GAG (TTT F	TTT F	CTG L	AAT N	TCA S	CCA P	GTT V	AAG K	GCC	GAT D
SCCA	s cAG	GGT	GTG /	GAT	GGA	AAG K	SCG P	AAT N	AGA R	CGT R	AAG K	GAG E	GAT D	CCT P
າດດດດ	A ATG M	AAG (AAT (GTC	TCT	CAT H	GTT V	TCC S	CTT L	ATG M	GAT D	GGA G	AGG R	CCA P
rtti	aaaa	ACG T	TTT	TCT	000 P	ATG M	GTT V	CGT R	GAA	9 999	GAG E	TGT C	ATC	ATA I
AAA.	rtcc	ACT	CGA R	A A A	CTG L	ATT I	GAT D	ن الدالدال	GCT	CCA P	AAG K	GTT V	CGA R	CAC
. 9395	ACAA'	900	CCA	TCG S	GTC V	AAT N	GAA E	CAA	AGA R	ACA T	TTT F	CCG P	TCT	TTA L
3CAA(rctc	929 8	GGA	GTT V	CGT R	TCC S	CGA R	CCT P	ე ე	GAA E	ACT	GAT D	TCT S	ACC T
CGAC	rctc	ACC T	GGA	GCT A	CGT R	TTC F	AGC S	A'I'ſ I	AGT S	CCA P	ATG	CAG Q	GAG E	AAG K
rcta(rcac)) ()	AGC	TTT F	CCG	CTG L	AGG R	GTT V	TTC F	GGT G	GAA E	CTC L	CTT L	AGA R
CATT	rctc	AAA K	ວ <u>ອ</u>	cgt R	GTT V	TCC S	GAG E	GA'I' D	AGT S	CCT P	GAT D	ATG M	TGG W	GAT D
0000	ITTC'	CAA	ე ე	GTA V	AAG K	TCG S	GGA G	AA'I'	TTT F	GTT V	gag E	A A	GAA E	TAC
3TTT(ATCG'	TTC (999 9	TCT	GAG E	GCT A	TCT S	GCT A	GCT A	GAT D	CTG L	CTG L	TTT F	CTT L
ratc	AAAC!	TTC '	၁ ၁ ၁ ၁	GCT A	CCG P	GAT D	TGT C	AAG K	CAT H	ე ეენე	GTT V	AGG R	A A	CCC P
SGAG	CTCA	TCT	AGC		CCA P	GST G	GAT D	ATG M	A.A.C.	GAT D	CGA R	A.A.A.	ACC	GAT D
CTGA(rcag(TTG		၁၅၅	ACT T	225 A	CGA R	TGT C	AGA R	GTA V	AAG K	AAC	GGA	GAT D
AGCCCTGAGGAGTATCGTTTCCGCCATTTCTACGACGCAAGGCGAAATTTTTGGCGCCAATCTTTCCCCCC	TCTCTCAGCTCAAAACATCGTTTCTCTCTCTCTCTCTCACAATTCCAAAAA	ATT		4	GAT	TCC S	GAT D	CTA L	GAA E	GGA G	TTG	TCT	GAA	CCT P
ነ ተሞቤ	SAAT	TCG 1					GAT D		CAA	ATA I				
B B B B G T T G	TTTCGAAT	AGA 1						TCA	ACT	GAT	TCT	TTG L	GTA V	AGA R
-	1 18	_						514	574 145	634 165	694 185	754	814	874 245

934 265	AAG AAA ATG K K M	X X	_	rcr s	SCA T	rca c s	CAY A	AAG C K	CAA T	rat t Y	TGG A	AGT G	GTT A V	AAG A	AGT G	SAA TE	Y I	ο Σ Σ	AC A	TT I	993 284
996 285	GTG V	CTT L	TTC	TTT F	AAA K	GTG V	999 999	AAA K	TTT F	TAT Y	GAG E	CTG L	TAT Y	GAG	CTA	GAT C	928 A	GAA	TTA	GGT G	1053 304
1054 305	CAC H	A.A.G K	GAG E	CTT L	GAC	TGG ¥	AAG K	ATG M	ACC T	ATG M	AGT S	GGT	GTG V	GGA	AAA	TGC A	AGA (CAG (GTT V	GGT G	1113 324
1114 325	ATC	TCT	GAA E	AGT S	999 9	ATA I	GAT D	GAG E	GCA A	GTG V	CAA	AAG	CTA	TTA	GCT A	CGT C	GGA S	TAT	X AA	GTT V	1173 344
1174 345	GGA	CGA R	ATC I	GAG	CAG	CTA	GAA	ACA	TCT	GAC	O CAA	GCA	¥ ¥	225	AGA (GGT C	GCT /	AAT	ACT	ATA I	1233 364
1234 365	ATT I	CCA P	AGG R	AAG K	CTA L	GTT V	CAG Q	GTA V	TTA L	ACT T	CCA P	TCA	ACA	GCA	AGC S	GAG (GGA 1	AAC	ATC I	999	1293 384
1294 385	CCT	GAT D	000 4	GTC V	CAT H	CTT	CTT	GCT A	ATA I	AAA K	GAG	ATC	X X	ATG	GAG (CTA C	CAA	AAG '	TGT	TCA	1353 404
1354 405	ACT	GTG V	TAT Y	GGA	TTT F	GCT A	TTT F	GTT V	GAC	TGT C	GCT	gcc A	TTG	AGG R	TTT '	TGG W	GTT (TCC	ATC . I	1413 424
1414	AGC S	GAT D	GAT D	GCA A	TCA S	TGT C		GCT A	CIT L	g GGA	GCG A	TTA	TTG .	ATG	CAG	GTT 1	rcr (CCA 1	AAG K	GAA E	1473
1474	GTG V	TTA L	TAT Y	GAC D .	AGT	A AAA	999	CTA L	TCA S	AGA R	GAA	GCA A	CAA	AAG K	GCT (CTA P	AGG 1	AAA 7	TAT	ACG T	1533 464
1534 465	TTG L	ACA T	ე ე	TCT	ACG T	929 A	GTA	CAG Q	TTG L	GCT A	CCA P	GTA V	CCA (CAN	GTA 1	ATG G M	9 999	GAT A	ACA	GAT D	1593 484
1594 485	GCT A	GCT A	GGA G	GTT	AGA R	AAT N	ATA I	ATA I	GAA	TCT S	MAC	. V55	TAC	TTT	AAA O	GGT 1	rcr 1	TCT (S	GAA	TCA S	1653 504
1654 505	TGG W	AAC N	TGT C	GCT A	GTT V	GAT D	GGT G	CTA	AAT	GAA E	TGT	GAT (GTT (9 229 P	CTT /	AGT G	GCT C	CTT (GGA 6	GAG E	1713 524
1714 525	CTA L	ATT I	AAT N	CAT H	CTG L	TCT S	AGG R	CTA	AAG	CTA	GAA C	GAT (GTA O	CTT /	AAG C	CAT G	999	GAT A	ATT	TTT F	1773 544
1774 545	CCA P	CCA TAC P Y	CAA	GTT V	TAC Y	AGG R	GGT	TGT	CTC	AGA ATT R I Figure		GAT (D) (C)	GGC G nti	CAG 1 0 1 nued)	ACG A	ATG G M V	GTA P	AAT O	CTT (GAG E	1833 564

1893 584	1953 604	2013 624	2073	2133 664	2193 684	2253 704	2313 724	2373 744	2433 764	2493 784	2553 804	2613 824	2673 844	2733 864
A.A.C.	GAT D	AGT S	CGC R	CTC V	GAT D	AAA K) d V	ACT T	. CAC H	SGA G	ACA T	r ggr g	-	r cGT R
GAT D	X A	gaa E	GGA G	X X	ATT I	767 C	GCA A	GAA E	ATT I	GCT A	A A A	GAT D	S S	CTT
CTT L	CTC L	TCA S	CTC L	X X	GGA G	CTC L	GAA E	GCT A	GTC V	TCT S	CAG Q	₽	၁၅၅	CTT L
TAT Y	CCA P	AAC N	CTG L	ეეე ეეე	AGT S	A A	TTC F	AAC N	GAG E	CTC	AAT N	GCA A	AGT S	ACT
AAA K	CAT H	GCA A	AGA R	CTG L	AGA R	TAT Y	CAA Q	GAA E	TCT S	AGT S	CAG Q	GTT V	AGC S	TCA
TAC Y	TGC	ACG T	GAA	C'rT L	TTC F	CTT L	TCT S	GAT D	7.GG ₩	GCA A	GAT D	GCA	AGA R	AAA K
TTG L	ATC I	TTC F	T'ſÅ L	901 A	999	176 L	CTT I.	ACA T	CANA	GCA A	ACA T	TTT E	AGA R	GGA AV G K Inued)
ACC T	TGG W	GAA E	GAC D	CC.T P	X X	N.T. S	TTT F	GTG V	ACT T	ATC I	GCT A	CCA P	GCT A	GGC G
999	AAT'	GAA E	CCA P	TTG L	GTG V	V.Γ. Σ	TTA L	GAT D	GCA A	GCA A	GAA E	CAT H	GAG	ATG M
TCA	AGG R	GTT V	CTT	GTG V	ATT I	ATG M	GAG E	o cz	AGA R	TTT F	TCA	TGG W	<u> </u>	CCA AAC P N Figure
CCT	T'I'A L	GTA V	X X	TCT	CAA	AA'I' N	CTA L	AAC	GAA	TCT	GAA E	CTA L	CTT L	
GGT .	CTC L	GAT D	CAC H	000 V	0 0 0	TCA S	9 9 9	CAG Q	ATC 1	AGA	႕ သသ	GGA G	CTC L	GGA G
GGT	CGA	CTT L	CTC I.	TCA S	TTT F	GAA	AGC S	TAT Y	TTT F	CTG L	TTT F	CAA	ATA I	ACG
GAT	AAG K	CGG R	TAT Y	TCA	GCA A	AAG K	A AAA	AAT N	CTT L	GTC V	ATT	ATC I	GAT D	CTG L
TGT	GGT	A A A	CAG Q	CGA R	A.A.A	CAG Q	GGA G	CCA P	GAA E	GAT D	GTT	A A A	AAT	TTA L
AGC '	ACT T.	AAT N	၁၁၁	GTT V	GTT V	CTA	GTA V	TTT F	ATC I	CTA L	CCT P	CTT L	ა	TTG L
AAT N	CCA .	ATC	ACT	AGC S	CGA R	GCT A	TTA L	GAC	CTT L	1GC C	AGG R	ATA I	GTT V	TCA S
AAC 1	AGT (AGC S		TCT	CAA	TTG L	ATA I	AGC S	ATA I	AGC S	8 8	CCA P	CCT	000 8
TTT A		GAA 1			A A	TTG L	CCT P		ACA T	ATA I	ATG M	9 999	TTG L	CCT
ATA 1 I		GTA (CTG L					AGC S	A.A.A	CAA O	CAT H
.834 565					2134 665	2194 685	2254 705	2314	2374	2434 765	2494	2554 805	2614 825	2674 845

2793 884	2853 904	2913 924	2973 944	3033 964	3093 984	3153 1004	3213 1024	3273 1044	3333 1064	3393 1084	3453 1104	3521 5	3579 19	3606 28
TGC C	ACA T	ACT T	TAC Y	TTT E	AAA K	GAC	GTG V	GCC A	AGT	000 4	TCT S	TAA CACTATCTGAAGCTCGTTAAGTCTTTTGCCTCTCT	AAA K	
TCT	ATG M	GCA A	GGA G	CTC L	TCG S	CAA O	C. A.	CAA	TCA S	AAT N	TCC	SCCT	TTA A L K	
GAG E	ATC I	AAT N	GAT D	ATG M	ACC	GAT D	CTT L	GCT A	TTC F	AAC N	AAA K	ltt.	CGA T	
TGT	AGA R	CAG Q	TTC F	CGG R	GTC V	TGT C	GGA G	GCT	GAG E	CAC	ATC I	AGTCI	CCT CC	
000 P	GAT D	CTT	ACT T	TGT	CGT R	GGT G	TAC Y	GGT G	TCT S	gcc A	gag E	STTA	TTT CO	
GTG V	TCT	GTT V	AGT S	CAA	CCA P	CGT R	AGC S	TCA	AGA R	GTC V	CAT H	SCTC	TTG TT L F	=
TAC	GCA A	TCA S	ACT T	GTT V	CAC H	CCA P	GAG E	GCA	CTA	CGA R	TGG ₩	rgaac	AAA TI K L	(C ntinued)
1GC	၁၉၅	GCG A	GGA G	A A	TCT S	CAA	CCT P	ACA T	GAG E	TCT S	TTA L	ratci	AAA AA K	nti
၁၅၅	CTT L	ACA T	AGA R	GAG E	GCG	TAT Y	TGT C	GAA E	AGT' S	ATT I	1GC C	CAC	ATC A	
CTT	AGG R	GAG E	၁၁၅	GTA V	TTC F	GAT D	GCT	GT'ľ V	TCA S	GGT G	TTT F	TAA	TAT AY Y I	Figure 9
CAA	ACA T	ACT T	CTG L	CTG L	GAA E	TCT	GGA G	GTG V	AAG K	GTG V	TTG L	ACA T	TTA T/ L Y	
SCC A	TTC	TGC	GAA	CAC H	AAG K	AGA R	GAG E	CAA	TTC F	TTG L	ACT T	ATG M	TGC T' C L	A A A A
1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	ATC I	GAA E	GAC D	CGT R	ACC T	TCA S	ACC T	AAC N	AAC	TCA	GAC D	GCT	AAA TO	AAA K
ATC I	ACT	GTA V	CTT L	TTT F	CTC L	AAA K	TTA L	CCA P	GC;A	A.A.G K	TAC	ATG M	AAA AV K	AAA K
GTT V	GAT D	TTG L	ATC I	GTT	CCT P	TTC F	CGT R	ATA I	ე ეეე	CTC	GAC	TAA	CTT A	K AA
9 8 8	GTG V	tțt F	GTA V	TCG S	CAC H	GCA	TAC Y	GGA G	ATT I	TGG W	GAT D	AAA K	CCT C	X X
CTG L	CTC L	ACC T	CTA L	TAC Y	TAC Y	76C C	TTG L	GCT A	TCA S	GAC	GAA E)) •	ATT CO	AAA AAA K K
TGT			TCA	GCA A	CAT H	GCT A	TTC F	C ATG	AGA R	Ω EAA	၁၅၅	GTT V	TTT A	A A
	ATC I		GAT D				GTG V	CTC L	AAG K	CAT H	ATT I	TGT C	ATG T	A AA
	GAA	GGA G	CAG	၁၁၅ န	GCA					CTG L) 200	TAC	S A M	AAA K
2734 865	2794 885	2854 905	2914 925	2974 945	3034 965	3094 985	3154 1005	3214 1025	3274 1045	3334 1065	3394 1085	3454 1105	3522	3580

=	
-	
<u>ဗ</u>	
3	
권)
Ξ.	



	50
TTTTTTGGTTGCTAACAATAAAGGTATACGGTTTTATGTCATCAATATAA	100
CTATATATAAAAGAAATGAAAGATATATATTGTTTTTTCATTTATCAAAC	150
AAAACAACAAGACTTTTTTTTTTTTTTTTTTTTTTTTTT	200
GATAAACGACATCGTTTAATCATTTCCCAATTTTACCCCTAAGTTTAACA	250
CCTAGAACCTTCTCCATCTTCGCAAGCACAGCCTGATTAGGAACAGCTTT	300
ACCATTCTCATATTCCTGAACTACCTGAGTCCTCTCATTGATCTGTTTCG	350
CCAAATCCGCTTGTGACATCTTCTTCTCCAATCTCGCTTTCTGTATCATC	400
AACCTCACCTCTGCTTTCACACGATCCATCGCCGCAGGCTCTGTTTCTTC	450
TTCCAGCTTCTTCGTGTTAATCACCGGGAACCGCCGTAGATTTCCCCTTTT	500
TGTTCGAACCGGCATCGAATTTCTTAACCGTTTGAACCGCGACACCGTTT	550
CTCAGAGCTGCGTTAACCGCTTTCGGATCGCGTAGGTCTTGGCTCTTTTG	600
TTTTGATTTGTGGAGAACTACTGGTTCCCAGTCTTGTGTTACTGCTCCTG	
GGTATCTGCTCGGCATCGATGAATTGAGAGAAAGGAACAACGCGAAA	650
ATTTTATTAATCTGAGTTTTGAAATTGAGAAACGATGAAGATGAAGAATG	700
TTGTTGAGAGGATTGTGATATTATATATACGAAGATTGGTTTCTGGAGA	750
ATTCGATCATCTTTTCTCCATTTTCGTCTCTGGAACGTTCTTAGAGATG	800
ATTGACGACGTGTCATTATCTGATTTGCAGTTAACCAATGCTTTTTGGGT	850
TGGATTCGTGGTACACCATATTATCCGATTTGGCTCAATGGTTTTATATA	900
AATTTGGTTTTCGGTTCGGTTATGAGTTATCATTAAAATTAAGCTAACCA	950
AAAATTTTCGTAAAATTTATTTCGGTTTCAATTCGGATCCCTTACTTCCA	1000
GAACCGAATTATTCGAAACCGGGGTTAGCCGAACCGAATACCAATGCCTG	1050
ATTGACTCGTTGGCTAGAAAGATCCAACGGTATACAATAATAGAACATAA	1100 1150
ATCGGACGGTCATCAAAGCCTCAAAGAGTGAACAGTCAACAAAAAAAGTT	1200
GAGCCCTGAGGAGTATCGTTTCCGCCATTTCTACGACGCAAAGGCGAAAAT	1250
TTTTGGCGCCAATCTTTCCCCCCTTTCGAATTCTCTCAGCTCAAAACATC	1300
GTTTCTCTCTCACTCTCTCACAATTCCAAAAAATGCAGCGCCAGAGAT	1350
CGATTTTGTCTTCCTAAAAACCCACGGCGGCGACTACGAAGGGTTTG	1400
GTTTCCGGCGATGCTGCTAGCGGCGGGGGGGGGCAGCGGAGACCACGATTT	1450
AATGTGAAGGAAGGGGATGCTAAAGGCGACGCTTCTGTACGTTTTGCTGT	1500
TTCGAAATCTGTCGATGAGGTTAGAGGAACGGATACTCCACCGGAGAAGG	1550
TTCCGCGTCGTGTCCTGCCGTCTGGATTTAAGCCGGCTGAATCCGCCGGT	- ·
GATGCTTCGTCCCTGTTCTCCAATATTATGCATAAGTTTGTAAAAGTCGA	1600
TGATCGAGATTGTTCTGGAGAGAGGTACTAATCTTCGATTCTCTTAATTT	1650
TGTTATCTTTAGCTGGAAGAAGAATTCGTGTAATTTGTTGTATTCGTT	1700
GGAGAGATTCTGATTACTGCATTGGATCGTTGTTTACAAATTTTCAGGAG	1750
CCGAGAAGATGTTCCCCCTGAATGATTCATCTCTATGTATG	1800
ATGATGTTATTCCTCAATTTCGTTCCAATAATGGTAAAACTCAAGAAAGA	1850
AACCATGCTTTTAGTTTCAGTGGGAGAGCTGAACTTAGATCAGTAGAAGA	1900
TATAGGAGTAGATGGCGATGTTCCTGGTCCAGAAACACCAGGGATGCGTC	1950
CACGTGCTTCTCGCTTGAAGCGAGTTCTGGAGGATGAAATGACTTTTAAG	2000
GAGGATAAGGTTCCTGTATTGGACTCTAACAAAAGGCTGAAAATGCTCCA	2050
GGATCCGGTTTGTGGAGAGAAGAAGAAGTAAACGAAGGAACCAAATTTG	2100
AATGGETTGAGTCTTCTCGAATCAGGGATGCCAATAGAAGACGTCCTGAT	2150
GATCCCCTTTACGATAGAAAGACCTTACACATACCACCTGATGTTTTCAA	2200

Figure 11

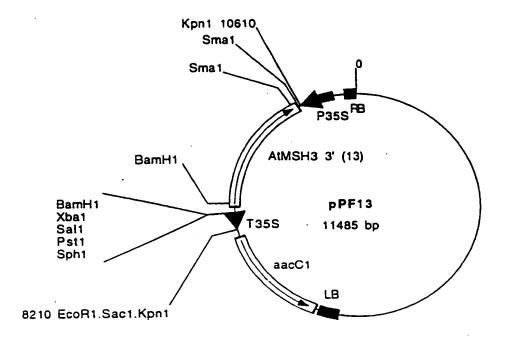
GAAAATGTCTGCATCACAAAAGCAATATTGGAGTGTTAAGAGTGAATATA	2250
GAAAATGTCTGCATCACAAAAGCAATATTGGAGTGTTATAATCTAGTGTT TGGACATTGTGCTTTCTTTAAAGTGGTTAGTAACTATTAATCTAGTGTT	2300
TGGACATTGTGCTTTTCTTTAAAGTGGTTAGTATCTTTTACGTTATG CAATCCATTTCCTCAATGTGATTTGTTCACTTACATCTGTTTACGTTATG	2350
CAATCCATTTCCTCAATGTGATTTGTTCACTTTGTTCTCTTTGTTCCCGGAATTAG	2400
CTCTTCTCAGGGGAAATTTTATGAGCTGTATGAGCTTGTTGTGTGTG	2450
GTCACAAGGAGCTTGACTGGAAGATGACCATGAGTGGTGTGTGT	2500
AGACAGGTAAATTAGTTGAAACAACTGGCCTGCTTGAATTATTGTGTCTA	2550
TAAATTTTGACACCACCTTTTGTTTCAGGTTGGTATCTCTGAAAGTGGGA	2600
TAGATGAGGCAGTGCAAAAGCTATTAGCTCGTGGGTAAGGGAACCATCAT	2650
ACTTTATGGAATTCGTTTACTGCTACTTCGGCTAGGATTTAAGAAATGGA	2700
AATCACTTCAAGCATCATTAGTTAGGATCCTGAGAACTCAGGATGTTTTC	2750
TTATTCGTTATATAATAAGTCTTTTCATCAAGGAGTAACAAACA	2800
GCACAATATTTGTGTGCTCACTGGCAAGGCATATATACCCAGCTAACCTT	2850
TGCTAGTTCACTGTAGTAACAGTTACGGATAATATATGTTTACTTGTATG	2900
TGGTACCCTCATTTTGTCTCTCATGGAGGCTTTCAAGCCTTGTGTTGAAA	2950
CTGGATAGTTACATATGCTTCCAACAGAAACTAGCATGCAGATTCATATG	3000
CTTTCCTATTCTACTAATTATGTATTGACACACTCGTTGTTTCTTTTGAA	3050
AGATATAAAGTTGGACGAATCGAGCAGCTAGAAACATCTGACCAAGCAAA	3100
AGCCAGAGGTGCTAATACTGTAAGTTTTCTTGGATAGGTCAAGGAGAGTG	3150
TTGCAGACTGTTTTTGATCATTTCTTTTTTTTGTACATTACTTTCATGCTG	3200
TAATTAACTCAATGGCTATTCTGGTCTGATTATCAGATAATTCCAAGGAA	3250
GCTAGTTCAGGTATTAACTCCATCAACAGCAAGCGAGGGAAACATCGGGC	3300
CTGATGCCGTCCATCTTCTTGCTATAAAAGAGGTTTGTTATTTACTTATT	3350
TATCTTATCATGTTCAGTTCATCCAAGTCCTGAAAAATTACACTCTTCTT	3400
TACCAATCTTCCATCAAGCTGTGTAAAGGATTTGGAATTAGAAAATCATT	3450
ATTTGATGCTTTGTTTTATATGCAAGAGGTTCCCTTGAAAAGATCTGTTT	3500
AAGATTCTTTGCACTTGAAAAATTCAATCTTTTTAAGTGAATCCCCTACT	3550
TTCTTACAATGATCATAGTCTGCAATTGCATGTCAAGTAATATCATTCCT	3600
TGTTACTGCATCCCCCTCTTTCTTAATGACCATTGTCTATGTTGTGTTTTG	3650
TCTCGTGTGCTGGAGAAATGATAGCTGATCCAAGCTGTACATTATCATG	3700
ATTAAGTAGCTGCTCAGGAATTGCCTTTGGTTACATTGCCTAATGGTTTG	3750
ATGTCAATTTTCTTCTGAATCTTTATTTTAGATCAAAATGGAGCTACAA	3800
AAGTGTTCAACTGTGTATGGATTTGCTTTTGTTGACTGTGCTGCCTTGAG	3850
GTTTTGGGTTGGGTCCATCAGCGATGATGCATCATGTGCTGCTCTTGGAG	3900
CGTTATTGATGCAGGTAAGCAAGTGTATTCTGTATCTTATGTGTACCATG	3950
TGACTTCCTGTGCATATTTTGGGTTGCAGGAACTAATTCTGAATCACCA	4000
TTTGGTATGTTTTTCCAGGTTTCTCCAAAGGAAGTGTTATATGACAGTA	4050
AAGGTAAACTGCTTGTATCGCCAGTTGTTTTGTTAAACAGAATTTAAGGT	4100
AAATGACACTGGTTAATTTAAAGTGCATACATGTTGAAATATTGCAGGGC	4150
TATCAAGAGAAGCACAAAAGGCTCTAAGGAAATATACGTTGACAGGTACC	
ATTTCAGTAGGCAAGCTAACTGACAATTTAACCGCTCACCGAATGATAGG	4200 4250
TCTCTTAAACATTGCTAATGTAGATGATGTTTATGTTTCAATCTAATAGG	4250
GTCTACGGCGGTACAGTTGGCTCCAGTACCACAAGTAATGGGGGGATACAG	
ATGCTGCTGGAGTTAGAAATATAATAGAATCTAACGGATACTTTAAAGGT	4350 4400
TCTTCTGAATCATGGAACTGTGCTGTTGATGGTCTAAATGAATG	4400
•	

TGCCCTTAGTGCTCTTGGAGAGCTAATTAATCATCTGTCTAGGCTAAAGG	4450
TGTGTTGGCTTGTTTAGTTTTTGCTTTTCACAAATTAAGCAAAGGAACTT	4500
TTCATAACTTACAGTTTCTATCTACTTGCAGCTAGAAGATGTACTTAAGC	4550
ATGGGGATATTTTCCATACCAAGTTTACAGGGGTTGTCTCAGAATTGAT	4 600
GGCCAGACGATGGTAAATCTTGAGATATTTAACAATAGCTGTGATGGTGG	4650
TCCTTCAGGCAAGTGCATATTTCTTTTTTGATAACTTCAACTAGAGGGCA	4700
GACATAGAAGGAAAAATTCTAATACTTCGTACGGATCTCCAGTAAGTA	4750
AGCCGATTTTTGTTTACCTATGTAGGGACCTTGTACAAATATCTTGATAA	4800
CTGTGTTAGTCCAACTGGTAAGCGACTCTTAAGGAATTGGATCTGCCATC	4850
CACTCAAAGATGTAGAAAGCATCAATAAACGGCTTGATGTAGTTGAAGAA	4900
TTCACGGCAAACTCAGAAAGTATGCAAATCACTGGCCAGTATCTCCACAA	4950
ACTTCCAGACTTAGAAAGACTGCTCGGACGCATCAAGTCTAGCGTTCGAT	5000
CATCAGCCTCTGTGTTGCCTGCTCTTCTGGGGAAAAAAGTGCTGAAACAA	5 050
CGAGTAAGTATCAATCACAAGTTTTCTGAGTAATGCCTTCCATGAGTAGT	5100
ATAGGACTAAAACATTACGGGTCTAGCTAAAGACTGTTCTCCTTCTTTTG	5150
CAATGTCTGGTTATTCATTACATTTCTCTTAACTTATTGCATTGCAGGTT	5200
AAAGCATTTGGGCAAATTGTGAAAGGGTTCAGAAGTGGAATTGATCTGTT	5250
GTTGGCTCTACAGAAGGAATCAAATATGATGAGTTTGCTTTATAAACTCT	5300
GTAAACTTCCTATATTAGTAGGAAAAAGCGGGCTAGAGTTATTTCTTTC	5350
CAATTCGAAGCAGCCATAGATAGCGACTTTCCAAATTATCAGGTGCCCAT	5400
CTATCTTTCATACTTTACAACAAAATGTCTGTCACTACTCAAAGCAATGC	5450
ATATGGCTTAGATCTCAACTCACACCCCGAGGATCCTAAAGGGATTTGCT	5500
TTTTATTCCTAATGTTTTTGGATGGTTTGATTTATTTCTAACTTGAACTT	5550
ATTAATCTTGTACCAGAACCAAGATGTGACAGATGAAAACGCTGAAACTC	5600
TCACAATACTTATCGAACTTTTTATCGAAAGAGCAACTCAATGGTCTGAG	5650
GTCATTCACACCATAAGCTGCCTAGATGTCCTGAGATCTTTTGCAATCGC	5700
AGCAAGTCTCTCTGCTGGAAGCATGGCCAGGCCTGTTATTTTTCCCGAAT	5750
CAGAAGCTACAGATCAGAATCAGAAAACAAAAGGGCCAATACTTAAAATC	5800
CAAGGACTATGGCATCCATTTGCAGTTGCAGCCGATGGTCAATTGCCTGT	5850
TCCGAATGATATACTCCTTGGCGAGGCTAGAAGAAGCAGTGGCAGCATTC	5900
ATCCTCGGTCATTGTTACTGACGGGACCAAACATGGGCGGAAAATCAACT	5950
CTTCTTCGTGCAACATGTCTGGCCGTTATCTTTGCCCAAGTTTGTATACT	6000
CGTTAGATAATTACTCTATTCTTTGCAATCAGTTCTTCAACATGAATAAT	6050
AAATTCTGTTTTCTGTCTGCAGCTTGGCTGCTACGTGCCGTGTGAGTCTT	6100
GCGAAATCTCCCTCGTGGATACTATCTTCACAAGGCTTGGCGCATCTGAT	6150
AGAATCATGACAGGAGAGAGTAAGTTTTGTTCTCAAAATACCAATTCCTC	6200
GAACTATTTACTCAGATTTTGTCTGATTGGACAAGGTGGTTTTGCTTTTT	6250
TTTAGGTACCTTTTTGGTAGAATGCACTGAGACAGCGTCAGTTCTTCAGA	6300
ATGCAACTCAGGATTCACTAGTAATCCTTGACGAACTGGGCAGAGGAACT	6350
AGTACTTTCGATGGATACGCCATTGCATACTCGGTAACCTGCTCTTCTCC	6400
TTCAACTTATACTTGTTGATCAACAAAAACATGCAATTCATTTTGCTGAA	. 6450
ACTTATTGATTTATATCAGGTTTTTCGTCACCTGGTAGAGAAAGTTCAAT	6500
GTCGGATGCTCTTTGCAACACATTACCACCCTCTCACCAAGGAATTCGCG	6550
TCTCACCCACGTGTCACCTCGAAACACATGGCTTGCGCATTCAAATCAAG	6600

Figure 11 (Continued)

ATCTGATTATCAACCACGTGGTTGTGATCAAGACCTAGTGTTCTTGTACC	6650
GTTTAACCGAGGGAGCTTGTCCTGAGAGCTACGGACTTCAAGTGGCACTC	6700
ATGGCTGGAATACCAAACCAAGTGGTTGAAACAGCATCAGGTGCTGCTCA	6750
AGCCATGAAGAGATCAATTGGGGAAAACTTCAAGTCAAG	6800
CTGAGTTCTCAAGTCTGCATGAAGACTGGCTCAAGTCATTGGTGGGTATT	6850
TCTCGAGTCGCCCACAACAATGCCCCCATTGGCGAAGATGACTACGACAC	6900
TTTGTTTTGCTTATGGCATGAGATCAAATCCTCTTACTGTGTTCCCAAAT	6950
AAATGGCTATGACATAACACTATCTGAAGCTCGTTAAGTCTTTTGCTTCT	7000
CTGATGTTTATTCCTCTTAAAAAATGCTTATATATCAAAAAATTGTTTCC	7050
TCGATTATAACAAGATTATATGTATCTGTCGGTTTAGCTATGGTATAT	7100
AATATATGTATGTTCATGAGATTGGTCAAGAGAAATACTCACAAACAGTA	. 7150
TATTAAGAAGGAAATATGTTTATGCATTAATTTAAGTTTCAAGATAAACT	7200
GCAAATAACCTCGACTAAAGTTGCAAAGACCAAACACAAATTACAAAACT	7250
TATAAGACTTAAGTTCTGAATTCCCTAAAACCAAAAAAAA	7300
TATTTTGTTGCATCTACAAACAACACAAACCTACATAGTTTATAACTTAC	7350
TCATCACTGAGATTAACATCAGAATCATTCTCCATTTCTTCATCTTCACT	7400
CTCATCATCACCACCACCATGATGATTCTCCTCCTCTTCACGTAACC	7450
TAGCAATCTCACTCTGAGCTCTATCAACAATCTGCTTCTTCTGCAACTCC	7500
AAATCTCTCTGAAAATCAGCTCTCATCTTCTCCAACTCCTTCATTTGCTC	7550
TTTCTTACTCTTCTCCATCTTCTCATAAACCTTCCCAAACCTCTCAACAG	7600
AATCCGCCAACATCTTATACGAAGCAGCGTCATTAACCTTCTTCCTCTCG	7650
TACTCAACCTCATCCTCATCCTCCTCCTCTTCAGAATCACCAGGACT	7700
ATCCATCATCTCATCAAACCCATTAGACTTATCTAAATAAA	7750
TCATAAACACAAACTCACCTGAATCAACACCACAAGCTAAACCTAAATCC	7800
GACTTGGGCGAAACACAAAGCAACATATCCAACTTATTGAAAAACGACCA	7850
TTTACTTGAACCTAAACCTGATTTCTCAACCTTAATCTTCTCTTTTCTAT	7900
ACTTCCTCTCAAGTCATCAATCATTCTCCTACATTGCGTCTCAGATTTC	7950
TCCATCCTTAGCTCCTCACTCACTTTCTCAGCTACTTCATTCCAATCCTC	8000
GTTCCTCAAACTCCTTCTACCCAATTGCAAAAACCTATCTCCCCAAACTT	8050
CAAGCAACACAA	8062

Figure 11 (Continued)



Comments/References: AtMSH3 3' side antisense : AtMSH3 3' (13 = 2104bp) from pUC18/13 Sal1/Sst1/T4 into pCW164 BamH1/T4 in Agrobacterium LBA44O4

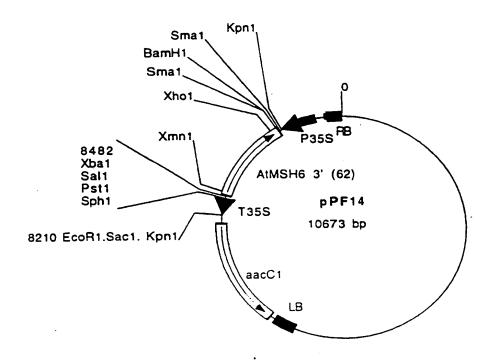


Figure 13

Comments/References: AtMSH6 (S8) 3' side antisens : 62 Sal1/Sst1/T4 (1379bp) into pCW164 BamH1/T4

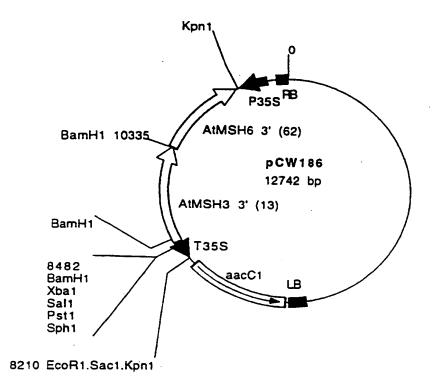


Figure 14

Comments/References: AtMSH6 3'/AtMSH3 3' antisense : AtMSH6 (S8) 3' side (62=1379bp) Sal1/Sst1/T4 into pPF13 (pCW164 AtMSH3 (S5) 3' side (13=2104) antisens)/Sma1. in LBA4404

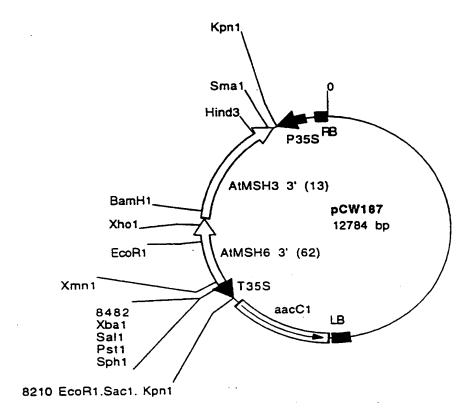


Figure 15

Comments/References: AtMSH3 3'/AtMSH6 3' antisens (D): AtMSH3 (S5) 3' side (13=2104bp) Sal1/Sst1/T4 into pPF14 (AtMSH6 (S8) 3'side (62=1379bp) antisense into pCW164)/Sma1. in LBA4404

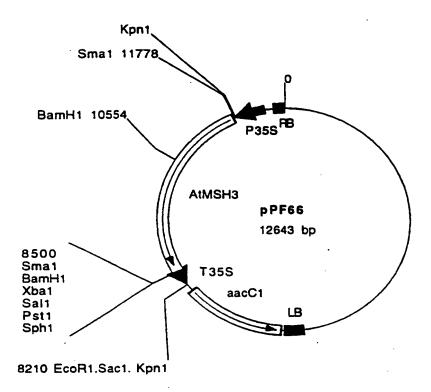


Figure 16

Comments/References: AtMSH3 (S8) complete, sense orientation : pPF26 (3342bp) Sma1 into pCW164 Sma1

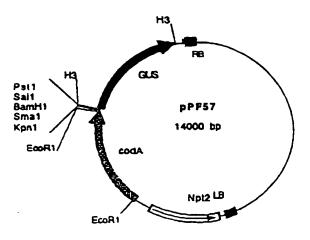
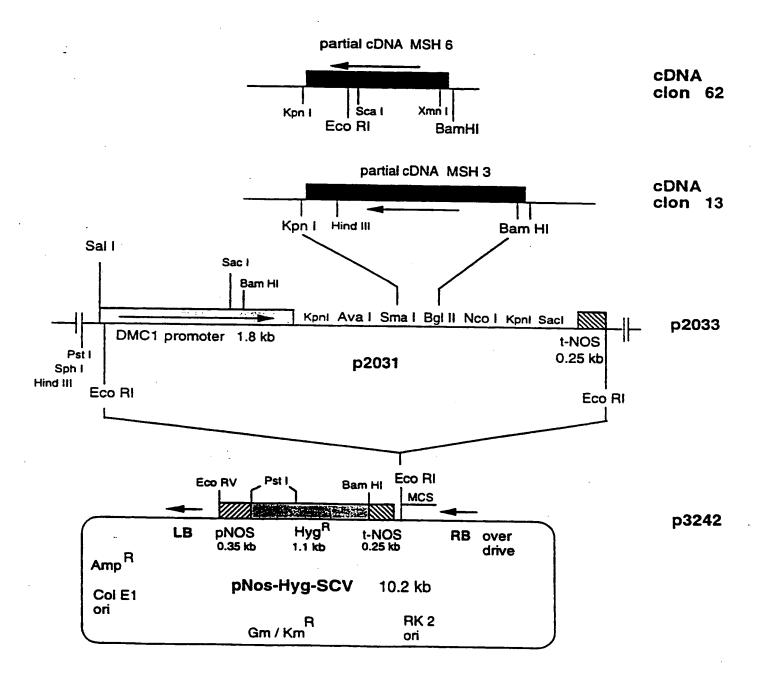
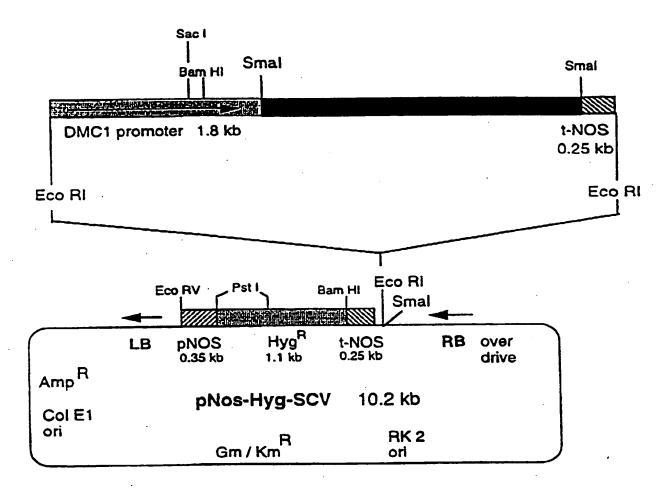


Figure 17

Comments/References: pPZP111 with codA EcoR1 cassette in EcoR1 site and HInd3 GUS cassette in Hind3 site. KanR. All genes under Promoter/terminator 35S



p3243



1

```
SEQUENCE LISTING
```

```
<110>
             Rhone-Poulenc Agro; Betzner, Andreas Stefan; Doutriaux,
             Marie-Pascale; Freyssinet, Georges; Perez, Pascual.
            Methods for obtaining plant varieties
<120>
<130>
            395498C
<150>
            PO9745
<151>
            1997-10-10
<160>
            98
<210>
            1
            23
<211>
<212>
            DNA
<213>
            Artificial sequence
<220>
<221>
            modified_base
<222>
            11
<223>
           I
<220>
<221>
            modified base
<222>
            14
<223>
            I
<220>
<221>
            modified base
<222>
            17
<223>
<220>
<223>
          Degenerate oligonucleotides UPMU used to isolate AtMSH3 and
            AtMSH6.
<300>
<301>
            Reenan and Kolodner
<302>
            Genetics
<303>
            132
<306>
            963-973
<307>
            1992
<400>
            1
ctggatccac nggnccnaay atg
                                                                      23
<210>
            2
<211>
            23
```

<212>

DNA

2

```
Artificial sequence
<213>
<220>
<221>
              modified base
<222>
              15
<223>
<220>
<221>
              modified base
<222>
              18
:<223>
 <220>
              Degenerate oligonucleotides DOMU used to isolate AtMSH3 and
 <223>
              AtMSH6.
 <300>
              Reenan and Kolodner
 <301>
 <302>
              Genetics
 <303>
              132
 <306>
              963-973
 < 3.07 >
              1992
 <400>
                                                                       . 23
 ctggatccrt artgngtnrc raa
 <210>
              3
 <211>
              24
 <212>
              DNA
              Artificial sequence
 <213>
 <220>
              MSH3 specific primer 636 for PCR using cDNA of Arabidopsis
 <223>
               thaliana ecotype Columbia
               3
 <400>
                                                                          24
 tgctagtgcc tcttgcaagc tcat
 <210>
               4
 <211>
               27
 <212>
               Artificial sequence
 <213>
 <220>
               Primer AP1 for PCR using cDNA of Arabidopsis thaliana ecotype
 <223>
               Columbia containing adapter sequences ligated to both its
               ends
  <400>
```

-3

ccatcctaat	acgactcact atagggc 27
<210>	5
<211>	23
<212>	DNA
<213>	Artificial sequence
(223)	nacazaczna begnerec
<220>	
<223>	Primer AP2 for PCR using cDNA of Arabidopsis thaliana ecotype
	Columbia containing adapter sequences ligated to both its
	ends ends
400	
<400>	5
actcactata	gggctcgagc ggc 23
<210>	6
<211>	30
<212>	DNA ·
<213>	Artificial sequence
<220>	
<223>	MSH3 specific primer S525 for PCR using cDNA of Arabidopsis
<223>	thaliana ecotype Columbia
<400>	6
aggttctgat	tatgtgtgac gctttactta 30
<210>	7
<211>	29
<212>	DNA
<213>	Artificial sequence
<220>	\cdot
<223>	MSH3 specific primer S51 for PCR using cDNA of Arabidopsis
,	thaliana ecotype Columbia
<400>	7 ·
ggatcgggta	ctgggttttg agtgtgagg 29
<210>	8
<211>	24
<212>	DNA ·
<213>	Artificial sequence
	natalata seguence
<220>	
<223>	MSH3 specific primer 635 for PCR using cDNA of Arabidopsis
	thaliana ecotype Columbia

4

<400>	8	
gcacgtgctt	gatggtgttt tcac	24
<210> <211> <212> <213>	9 28 DNA Artificial sequence	
<220>		
<223>	MSH3 specific primer S523 for PCR using cDNA of Arabidor thaliana ecotype Columbia	sis
<400>	9	
tcagacagta	tccagcatgg cagaagta	28
	,	
<210>	10	
<211>	33	
<212>	DNA	
<213>	Artificial sequence	
(213)	Altilitat ocaucio	
<220>		
<223>	MSH3 specific primer 1S5 for PCR using cDNA of Arabidops thaliana ecotype Columbia	sis
<400>	10	
atcccgggat	gggcaagcaa aagcagcaga cga	33
210		
<210>	11	
<211>	27 DNA	
<212> <213>	Artificial sequence	
<213>	Artificial sequence	
<220>		
<223>	MSH3 specific primer S53 for PCR using cDNA of Arabidop thaliana ecotype Columbia	sis
<400>	11	
gacaaagago	gaaatgagge ceettgg	27
<210>	12	
<210>	1250	
<211> <212>	DNA	
<213> <223>	Arabidopsis thaliana ecotype Columbia Clone 52	
~ 4 4 4 7		

<400> 12

cccgggatgg	gcaagcaaaa	gcagcagacg	atttctcgtt	tcttcgctcc	caaacccaaa	60
tccccgactc	acgaaccgaa	tccggtagcc	gaatcatcaa	caccgccacc	gaagatatcc	120
gccactgtat	ccttctctcc	ttccaagcgt	aagcttctct	ccgaccacct	cgccgccgcg	180
tcacccaaaa	agcctaaact	ttctcctcac	actcaaaacc	cagtacccga	tcccaattta	240
caccaaagat	ttctccagag	atttctggaa	ccctcgccgg	aggaatatgt	tcccgaaacg	300
tcatcatcga	ggaaatacac	accattggaa	cagcaagtgg	tggagctaaa	gagcaagtac	360
ccagatgtgg	ttttgatggt	ggaagttggt	tacaggtaca	gattcttcgg	agaagacgcg	420
gagatcgcag	cacgcgtgtt	gggtatttac	gctcatatgg	atcacaattt	catgacggcg	480
agtgtgccaa	catttcgatt	gaatttccat	gtgagaagac	tggtgaatgc	aggatacaag	540
attggtgtag	tgaagcagac	tgaaactgca	gccattaagt	cccatggtgc	aaaccggacc	600
ggcccttttt	tesggggaet	greggegreg	tataccaaag	ccacgcttga	agcggctgag	660
gatataagtg	gtggttgtgg	tggtgaagaa	ggttttggtt	cacagagtaa	tttcttggtt	720
tgtgttgtgg	atgagagagt	taagtcggag	acattaggct	gtggtattga	aatgagtttt	780
gatgttagag	teggtgttgt	tggcgttgaa	atttcgacag	gtgaagttgt	ttatgaagag	840
ttcaatgata	atttcatgag	aagtggatta	gaggctgtga	ttttgagctt	gtcaccagct	900
gagctgttgc	ttggccagcc	tctttcacaa	caaactgaga	agtttttggt	ggcacatgct	960
ggacctacct	caaacgttcg	agtggaacgt	gcctcactgg	attgtttcag	caatggtaat	1020
gcagtagatg	aggttatttc	attatgtgaa	aaaatcagcg	caggtaactt	agaagatgat	1080
aaagaaatga	agctggaggc	tgċtgaaaaa	ggaatgtctt	gcttgacagt	tcatacaatt	1140
atgaacatgc	cacatctgac	tgttcaagcc	ctcgccctaa	cgttttgcca	tctcaaacag	1200
tttggatttg	aaaggatcct	ttaccaaggg	gcctcatttc	gctctttgtc		1250

<210> 13 <211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> MSH3 specific primer 2S5 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

13 <400> 34 attoogggto aaaatgaaca agttggtttt agto 14 <210> 27 <211> <212> DNA Artificial sequence <213> <220> MSH3 specific primer S52 for PCR using cDNA of Arabidopsis <223> thaliana ecotype Columbia <400> 14 27 gccacatctg actgttcaag ccctcgc 15 <210> 2110 <211> <212> Arabidopsis thaliana ecotype Columbia <213> Clone 13 <223> <400> 15 gecaeatetg aetgiteaag eedtegeeet aaegtittige eateteaaae agtitiggatt 60 tgaaaggate etttaceaag gggeeteatt tegetetttg teaagtaaca eagagatgae 120 tototoagoo aataototgo aacagttgga ggttgtgaaa aataattoag atggatogga 180 atotogotoc trattocata atatgaatoa cacacttaca gtatatggtt ccaggottot 240 tagacactgg gtgactcatc ctctatgcga tagaaatttg atatctgctc ggcttgatgc 300 tgtttctgag atttctgctt gcatgggatc tcatagttct tcccagctca gcagtgagtt 360 ggttgaagaa ggttctgaga gagcaattgt atcacctgag ttttatctcg tgctctcctc 420 480 agtettgaca getatgteta gateatetga tatteaaegt ggaataaeaa gaatetttea teggaetget aaageeacag agtteattge agttatggaa getattttae ttgeggggaa 540 600 gcaaattcag cggcttggca taaagcaaga ctctgaaatg aggagtatgc aatctgcaac tgtgcgatct actottttga gaaaattgat ttotgttatt toatcoootg ttgtggttga 660 720 caatgccgga aaacttctct ctgccctaaa taaggaagcg gctgttcgag gtgacttgct cgacatacta atcacttcca gcgaccaatt tcctgagctt gctgaagctc gccaagcagt 780 tttagtcatc agggaaaagc tggattcctc gatagcttca tttcgcaaga agctcgctat 840

tcgaaatttg	gaatttcttc	aagtgtcggg	gatcacacat	ttgatagagc	tgcccgttga	900
ttccaaggtc	cctatgaatt	gggtgaaagt	aaatagcacc	aagaagacta	ttcgatatca	960
tcccccagaa	atagtagctg	gcttggatga	gctagctcta	gcaactgaac	atcttgccat	1020
tgtgaaccga	gcttcgtggg	atagtttcct	caagagtttc	agtagatact	acacagattt	1080
taaggctgcc	gttcaagctc	ttgctgcact	ggactgtttg	cactcccttt	caactctatc	1140
tagaaacaag	aactatgtcc	gtcccgagtt	tgtggatgac	tgtgaaccag	ttgagataaa	1200
catacagtct	ggtcgtcatc	ctgtactgga	gactatatta	caagataact	tcgtcccaaa	1260
tgacacaatt	ttgcatgcag	aaggggaata	ttgccaaatt	atcaccggac	ctaacatggg	1320
aggaaagagc	tgctatatcc	gtcaagttgc	tttaatttcc	ataatggctc	aggttggttc	1380
ctttgtacca	gcgtcattcg	ccaagctgca	cgtgcttgat	ggtgttttca	ctcggatggg	1440
tgcttcagac	agtatccagc	atggcagaag	tacctttcta	gaagaattaa	gtgaagcgtc	1500
acacataatc	agaacctgtt	cttctcgttc	gcttgttata	ttagatgagc	ttggaagagg	1560
cactagcaca	cacgacggtg	tagccattgc	ctatgcaaca	ttacagcatc	tcctagcaga	1620
aaagagatgt	ttggttcttt	ttgtcacgca	ttaccctgaa	atagctgaga	tcagtaacgg	1680
attcccaggt	tctgttggga	cataccatgt	ctcgtatctg	acattgcaga	aggataaagg	1740
cagttatgat	catgatgatg	tgacctacct	atataagctt	gtgcgtggtc	tttgcagcag	1800
gagctttggt	tttaaggttg	ctcagcttgc	ccagatacct	ccatcatgta	tacgtcgagc	1860
catttcaatg	gctgcaaaat	tggaagctga	ggtacgtgca	agagagagaa	atacacgcat	1920
gggagaacca	gaaggacatg	aagaaccgag	aggcgcagaa	gaatctattt	cggctctagg	1980
tgacttgttt	gcagacctga	aatttgctct	ctctgaagag	gacccttgga	aagcattcga	2040
gtttttaaag	catgcttgga	agattgctgg	caaaatcaga	ctaaaaccaa	cttgttcatt	2100
ttgacccggg						2110

<210> 16
<211> 29
<212> DNA
<213> Artificial sequence
<220>

<223> MSH3 specific primer S51 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 16

ggatcgggta	ctgggttttg	agtgtgagg					29
<210>	17					•	
<211>	30						
<212>	DNA						
<213>	Artificia	l sequence					
<220>			_				
<223>		ecotype Co		or PCR us	sing cDN	A of Arab	ldopsis
<400>	17						
aggttctgat	tatgtgtgac	gctttactta					30
<210>	18						
<211>	3522						
<212>	DNA						
<213>	Arabidops	sis thalian	a ecotyp	e Columb	ia		
<220>							
<221>	CDS						
<222>	(100)	. (3342)					
<223>	AtMSH3 fr	ull-length	cDNA and	deduced	sequenc	e of the	encoded
	polypept:	ide					
<400>	18						
cctaagaaag	cgcgcgaaaa	ttggcaacco	aagttcg	cca tago	cacgac c	acgacctto	60
catttctctt	aaacggagga	gattacgaat	aaagcaa	itt .			99
מדם מסר ממ	g caa aag c	ag cag acg	att tct	cqt ttc	ttc gct	ccc aaa	147
Mer Gly Ly	s Gln Lys G	ln Gln Thr	Ile Ser	Arg Phe	Phe Ala	Pro Lys	
1	5		10	J		15	
ccc aaa to	c ccg act c	ас даа ссд	aat ccg	gta gcc	gaa tca	tca aca	195
	r Pro Thr H						•
FIO Dys Se	20	15 014 110	25		30		
ccg cca co	g aag ata t	cc gcc act	gta tcc	ttc tct	cct tcc	aag cgt	243
Pro Pro Pr	to Lys Ile S	er Ala Thr	Val Ser	Phe Ser	Pro Ser	Lys Arg	
3		40			45		
aag ctt ct	c tee gae e	ac ctc qcc	acc aca	tca ccc	aaa aaq	cct aaa	291
	eu Ser Asp H						
50	·· ·	55	-	60		•	
	ct cac act o						339
Leu Ser P	ro His Thr G	31n Asn Pro	Val Pro	Asp Pro	Asn Leu	His Gln	
65		70		75		80	

aga Arg	ttt Phe	ctc Leu	cag Gln	aga Arg 85	ttt Phe	ctg Leu	gaa Glu	ccc Pro	tcg Ser 90	ccg Pro	gag Glu	gaa Glu	tat Tyr	gtt Val 95	ccc Pro	387
gaa Glu	acg Thr	tca Ser	cca Ser 100	tcg Ser	agg Arg	aaa Lys	cac Tyr	aca Thr 105	cca Pro	ttg Leu	gaa Glu	cag Gln	caa Gln 110	gtg Val	gtg Val	435
gag Glu	cta Leu	aag Lys 115	agc Ser	aag Lys	tac Tyr	cca Pro	gat Asp 120	gtg Val	gtt Val	ttg Leu	atg Met	gtg Val 125	gaa Glu	gtt Val	ggt Gly	483
tac Tyr	agg Arg 130	tac Tyr	aga Arg	ttc Phe	ttc Phe	gga Gly 135	gaa Glu	gac Asp	gcg Ala	gag Glu	atc Ile 140	gca Ala	gca Ala	cgc Arg	gtg Val	531
ttg Leu 145	ggt	att Ile	tac Tyr	gct Ala	cat His 150	atg Met	gat Asp	cac His	aat Asn	ttc Phe 155	atg Met	acg Thr	gcg Ala	agt Ser	gtg Val 160	579
cca Pro	aca Thr	ttt Phe	cga Arg	ttg Leu 165	aat Asn	ttc Phe	cat His	gtg Val	aga Arg 170	aga Arg	ctg Leu	gtg Val	aat Asn	gca Ala 175	gga Gly	627
tac Tyr	aag Lys	att Ile	ggt Gly 180	gta Val	gtg Val	aag Lys	cag Gln	act Thr 185	gaa Glu	act Thr	gca Ala	gcc Ala	att Ile 190	aag Lys	tcc Ser	675
cat His	ggt Gly	gca Ala 195	aac Asn	cgg Arg	acc Thr	ggc	ect Pro 200	ttt Phe	ttc Phe	cgg Arg	gga Gly	ctg Leu 205	tcg Ser	gcg Ala	ttg Leu	723
tat Tyr	acc Thr 210	aaa Lys	gcc Ala	acg Thr	ctt Leu	gaa Glu 215	gcg Ala	gct Ala	gag Glu	gat Asp	ata Ile 220	agt Ser	ggt Gly	ggt Gly	tgt Cys	771
ggt Gly 225	.ggt Gly	gaa Glu	gaa Glu	ggt Gly	ttt Phe 230	ggt Gly	tca Ser	cag Gln	agt Ser	aat Asn 235	ttc Phe	ttg Leu	gtt Val	tgt Cys	gtt Val 240	819
gtg Val	gat Asp	gag Glu	aga Arg	gtt Val 245	aag Lys	tcg Ser	gag Glu	aca Thr	tta Leu 250	ggc	tgt Cys	ggt Gly	att Ile	gaa Glu 255	atg Met	867
agt Ser	ttt Phe	gat Asp	gtt Val 260	aga Arg	gtc Val	ggt Gly	gtt Val	gtt Val 265	ggc Gly	gtt Val	gaa Glu	att Ile	tcg Ser 270	aca Thr	ggt Gly	915
gaa Glu	gtt Val	gtt Val 275	Tyr	gaa Glu	gag Glu	ttc Phe	aat Asn 280	gat Asp	aat Asn	ttc Phe	atg Met	aga Arg 285	agt Ser	gga Gly	tta Leu	963

					Ser							ttg Leu				1	011
												cat Met				i	059
												tgt Cys				1	.107
												aaa Lys				1	.155
												gct Ala 365				נ	1203
gga Gly	atg Met 370	tct Ser	tgc Cys	ttg Leu	aca Thr	gtt Val 375	cat His	aca Thr	att Ile	atg Met	aac Asn 380	atg Met	cca Pro	cat His	ctg Leu	1	1251
act Thr 385	gtt Val	caa Gln	gcc Ala	ctc Leu	gcc Ala 390	cta Leu	acg Thr	ttt Phe	tgc Cys	cat His 395	ctc Leu	aaa Lys	cag Gln	ttt Phe	gga Gly 400	;	1299
ttt Phe	gaa Glu	agg Arg	atc Ile	ctt Leu 405	tac Tyr	caa Gln	Gly	gcc Ala	tca Ser 410	ttt Phe	cgc Arg	tct Ser	ttg Leu	tca Ser 415	agt Ser		1347
aac Asn	aca Thr	gag Glu	atg Met 420	act Thr	ctc Leu	tca Ser	gcc Ala	aat Asn 425	act	ctg Leu	caa Gln	cag Gln	ttg Leu 430	Glu	gtt Val		1395
gtg Val	aaa Lys	aat Asn 435	Asn	tca Ser	gat Asp	gga Gly	tcg Ser 440	Glu	tct Ser	ggc	tcc Ser	tta Leu 445	ttc Phe	cat His	aat Asn		1443
		His					Tyr					. Leu			tgg Trp		1491
	Thr					Asp					e Ser				gat Asp 480		1539
					e Ser					/ Sei					cag Gln		1587

11 .

ctc	agc Ser	agt Ser	gag Glu 500	t t g Le u	gtt Val	gaa Glu	gaa Glu	ggt Gly 505	tct Ser	gag Glu	aga Arg	gca Ala	att Ile 510	gta Val	tca Ser	1	635
cct Pro	gag Glu	ttt Phe 515	tat Tyr	ctc Leu	gtg Val	ctc Leu	tcc Ser 520	tca Ser	gtc Val	ttg Leu	aca Thr	gct Ala 525	atg Met	tct Ser	aga Arg	1	683
tca Ser	ser 530	gat Asp	att Ile	caa Gln	cgt Arg	gga Gly 535	ata Ile	aca	aga Arg	atc Ile	Phe 540	cat His	cgg Arg	act Thr	gct Ala	1	731
aaa Lys 545	gcc Ala	aca Thr	gag Glu	ttc Phe	att Ile 550	gca Ala	gtt Val	atg Met	gaa Glu	gct Ala 555	att Ile	tta Leu	ctt Leu	gcg Ala	999 999	1	779
aag Lys	caa Gln	att Ile	cag Gln	cgg Arg 565	ctt Leu	ggc Gly	ata Ile	aag Lys	caa Gln 570	gac Asp	tct Ser	gaa Glu	atg Met	agg Arg 575	agt Ser	1	827
atg Met	caa Gln	tct Ser	gca Ala 580	act Thr	gtg Val	cga Arg	tct Ser	act Thr 585	ctt Leu	ttg Leu	aga Arg	aaa Lys	ttg Leu 590	att Ile	tct Ser		875
gtt Val	att Ile	tca Ser 595	tcc Ser	cct Pro	gtt Val	gtg Val	gtt Val 600	gac Asp	aat Asn	gcc Ala	gga Gly	aaa Lys 605	ctt Leu	ctc Leu	tct Ser	1	923
gcc Ala	cta Leu 610	aat Asn	aag Lys	gaa Glu	gcg Ala	gct Ala 615	gtt Val	cga Arg	ggt Gly	gac Asp	ttg Leu 620	ctc Leu	gac Asp	ata Ile	cta Leu	1	971
atc Ile 625	act Thr	tcc Ser	agc Ser	gac Asp	caa Gln 630	ttt Phe	cct Pro	gag Glu	ctt Leu	gct Ala 635	gaa Glu	gct Ala	cgc Arg	caa Gln	gca Ala 640	2	019
gtt Val	tta Leu	gtc Val	atc Ile	agg Arg 645	gaa Glu	aag Lys	ctg Leu	gat Asp	ser 650	tcg Ser	ata Ile	gct Ala	tca Ser	ttt Phe 655	cgc Arg		067
aag Lys	aag Lys	ctc Leu	gct Ala 660	att Ile	cga Arg	aat Asn	ttg Leu	gaa Glu 665	ttt Phe	ctt Leu	caa Gln	gtg Val	tcg Ser 670	elà aaa	atc Ile	2	115
aca Thr	cat His	ttg Leu 675	ata Ile	gag Glu	ctg Leu	ccc Pro	gtt Val 680	gat Asp	tcc Ser	aag Lys	gtc Val	cct Pro 685	atg His	aat Asn	tgg Trp	2	163
gtg Val	aaa Lys 690	gta Val	aat Asn	agc Ser	acc Thr	aag Lys 695	aag Lys	act Thr	att [°] Ile	cga Arg	tat Tyr 700	cat His	ccc Pro	cca Pro	gaa Glu	2	211

	-	-			-	_		gct Ala		_						2259
								agt Ser			_	-				2307
			_		_	_	_	gtt Val 745		-		_	_	_	_	2355
_	_							tct Ser						-	. –	2403
Pro	Glu 770	Phe	Val	Asp	Asp	Cys 775	Glu	cca Pro	Val	Glu	11e 780	Asn	Ile	Gln	Ser	2451
	_							ata Ile			_			_		2499
Asn	Asp	Thr	Ile	Leu 805	His	Ala	Glu	GJÀ aaa	Glu 810	Tyr	Cys	Gln	Ile	11e 815	Thr	2547
			_	Gly	-			tgc Cys 825								2595
			_	-	_	Val		tcc Ser								2643
								ttc Phe				Gly				2691
_		_			_	_		ttt Phe			-		_	_		2739
				_		-		tct Ser	_	_		_			-	2787
			_			_		cac His 905			-	_		_		2835

gca aca tta cag cat ctc cta gca gaa aag aga tgt ttg gtt Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val 915 920 925	
gtc acg cat tac cct gaa ata gct gag atc agt aac gga ttc Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe 930 935 940	cca ggt 2931 Pro Gly
Ser Val Gly Thr Tyr His Val Ser Tyr Leu Thr Leu Gln Lys 945 950 955	
ggc agt tat gat cat gat gat gtg acc tac cta tat aag ctt Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu 965 970	
ggt ctt tgc agc agg agc ttt ggt ttt aag gtt gct cag ctt Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Gln Leu 980 985 990	
ata cct cca tca tgt ata cgt cga gcc att tca atg gct gca Ile Pro Pro Ser Cys Ile Arg Arg Ala Ile Ser Met Ala Ala 995 1000 1005	
gaa gct gag gta cgt gca aga gag aga aat aca cgc atg gga Glu Ala Glu Val Arg Ala Arg Glu Arg Asn Thr Arg Met Gly 1010 1015 1020	
gaa gga cat gaa gaa ccg aga ggc gca gaa gaa tct att tcg Glu Gly His Glu Glu Pro Arg Gly Ala Glu Glu Ser Ile Ser 1025 1030 1035	
ggt gac ttg ttt gca gac ctg aaa ttt gct ctc tct gaa gag Gly Asp Leu Phe Ala Asp Leu Lys Phe Ala Leu Ser Glu Glu 1045	
tgg aaa gca ttc gag ttt tta aag cat gct tgg aag att gct Trp Lys Ala Phe Glu Phe Leu Lys His Ala Trp Lys Ile Ala 1060 1065 1070	
atc aga cta aaa cca act tgt tca ttt tgatttaatc ttaacatta Ile Arg Leu Lys Pro Thr Cys Ser Phe 1075 1080	at 3362
agcaactgca aggtcttgat catctgttag ttgcgtacta acttatgtgt a	attagtataa 3422
caagaaaaga gaattagaga gatggattet aateeggtgt tgeagtacat (cttttctcca 3482
cccgcataaa aaaaaaaaa aaaaaaaaaa aaaaaaaaaa	3522

<210> 19 <211> 1081 <212> PRT

<213 <223					tide			a ec	осур	e co	CmD1	la			
< 400	>		19												•
Met 1	Gly	Lys	Gln	Lys 5	Gln	Gln	Thr	Ile	Ser 10	Arg	Phe	Phe	Ala	Pro 15	Lys
Pro	Lys	Ser	Pro 20	Thr	His	Glu	Pro	Asn 25	Pro	Val	Ala	Glu	Ser 30	Ser	Thr
Pro	Pro	Pro 35	Lys	Ile	Ser	Ala	Thr 40	Val	Ser	Phe	Ser	Pro 45	Ser	Lys	Arg
Lys	Leu 50	Leu	Ser	Asp	His	Leu 55	Ala	Ala	Ala	Ser	Pro 60	Lys	Lys	Pro	Lys
Leu 65	Ser	Pro	His	Thr	Gln 70	Asn	Pro	Val	Pro	Asp 75	Pro	Asn	Leu	His	Gln 80
Arg	Phe	Leu	Gln	Arg 85	Phe	Leu	Glu	Pro	Ser 90	Pro	Glu	Glu	Tyr	Val 95	Pro
Glu	Thr	Ser	Ser 100	Ser	Arg	Lys	Tyr	Thr 105	Pro	Leu	Glu	Gln	Gln 110	Val	Val
Glu	Leu	Lys 115	Ser	Lys	Tyr	Pro	Asp 120	Val	Val	Leu	Met	Val 125	Glu	Val	Gly
Tyr	Arg 130	Tyr	Arg	Phe	Phe	Gly 135	Glu	Asp	Ala	Glu	Ile 140	Ala	Ala	Arg	Val
Leu 145	Gly	Ile	Tyr	Ala	His 150	Met	Asp	His	Asn	Phe 155	Met	Thr	Ala	Ser	Val 160
Pro	Thr	Phe	Arg	Leu 165		Phe	His	Val	Arg 170	Arg	Leu	Val	Asn	Ala 175	Gly
Tyr	Lys	Ile	Gly 180	Val	Val	Lys	Gln	Thr 185	Glu	Thr	Ala	Ala	Ile 190	Lys	Ser
His	Gly	Ala 195	Asn	Arg	Thr	Gly	Pro 200	Phe	Phe	Arg	Gly	Leu 205		Ala	Let
Tyr	Thr 210	•	Ala	Thr	Leu	Glu 215		Ala	Glu	Asp	Ile 220		Gly	Gly	Cys
Gly 225	Gly	Glu	Glu	Gly	Phe 230		Ser	Gln	Ser	Asn 235		Leu	Val	Cys	Va]
Val	Asp	Glu	Arg	Val 245		Ser	Glu	Thr	Leu 250		Cys	Gly	lle	Glu 255	

Ser	Phe	Asp	Val 260	Arg	Val	Gly	Val	Val 265	Gly	Val	Glu	Ile	Ser 270	Thr	Gly
Glu	Val	Val 275	Tyr	Glu	Glu	Phe	Asn 280	Asp	Asn	Phe	Met	Arg 285	Ser	Gly	Leu
Glu	Ala 290	Val	Ile	Leu	Ser	Leu 295	Ser	Pro	Ala	Glu	Leu 300	Leu	Leu	Gly	Gln
Pro 305	Leu	Ser	Gln	Gln	Thr 310	Glu	Lys	Phe	Leu	Val 315	Ala	Met	Ala	Gly	Pro 320
Thr	Ser	Asn	Val	Arg 325	Val	Glu	Arg	Ala	Ser 330	Leu	Asp	Cys	Phe	Ser 335	Asn
Gly	Asn	Ala	Val 340	Asp	Glu	Val	Ile	Ser 345	Leu	Cys	Glu	Lys	Ile 350	Ser	Ala
Gly	Asn	Leu 355	Glu	Asp	Asp	Lys	Glu 360	Met	Lys	Leu	Glu	Ala 365	Ala	Glu	Lys
Gly	Met 370	Ser	Cys	Leu	Thr	Val 375	His	Thr	Ile	Met	Asn 380	Met	Pro	His	Leu
Thr 385	Val	Gln	Ala	Leu	Ala 390	Leu	Thr	Phe	Cys	His 395	Leu	Lys	Gln	Phe	Gly 400
Phe	Glu	Arg	Ile	Leu 405	Tyr	Gln	Gly	Alá	Ser 410	Phe	Arg	Ser	Leu	Ser 415	Ser
Asn	Thr	Glu	Met 420	Thr	Leu	Ser	Ala	Asn 425	Thr	Leu	Gln	Gln	Leu 430	Glu	Val
Val	Lys	Asn 435	Asn	Ser	Asp	Gly	Ser 440	Glu	Ser	Gly	Ser	Leu 445	Phe	His	Asn
Met	Asn 450	His	Thr	Leu	Thr	Val 455	Tyr	Gly	Ser	Arg	Leu 460	Leu	Arg	His	Trp
Val 465	Thr	His	Pro	Leu	Cys 470	Asp	Arg	Asn	Leu	11e 475	Ser	Ala	Arg	Leu	Asp 480
Ala	Val	Ser	Glu	11e 485		Ala	Cys	Met	Gly 490		His	Ser	Ser	Ser 495	Gln
Leu	Ser	Ser	Glu 500		Val	Glu	Glu	Gly 505		Glu	Arg	Ala	Ile 510		Ser
Pro	Glu	Phe 515	•	Leu	Val	Leu	Ser 520		Val	Leu	Thr	Ala 525		Ser	Arg
Ser	Ser	•	Ile	Gln	Arg	Gly		Thr	Arg	lle	Phe		Arg	Thr	Ala

Lys 545		Thr	Glu	Phe	Ile 550	Ala	Val	Met	Glu	Ala 555	Ile	Leu	Leu	Ala	Gly 560
Lys	Gln	Ile	Gln	Arg 565	Leu	Gly	Ile	Lys	Gln 570	Asp	Ser	Glú	Met	Arg 575	Ser
Met	Gln	Ser	Ala 580	Thr	Val	Arg	Ser	Thr 585	Leu	Leu	Arg	Lys	Leu 590	Ile	Ser
Val	Ile	Ser 595	Ser	Pro	Val	Val	Val 600	Asp	Asn	Ala	Gly	Lys 605	Leu	Leu	Ser
Ala	Leu 610	Asn	Lys	Glu	Ala	Ala 615		Arg	Gly	Asp	Leu 620	Leu	Asp	Ile	Leu
Ile 625	Thr	Ser	Ser	Asp	Gln 630	Phe	Pro	Glu	Leu	Ala 635	Glu	Ala	Arg	Gln	Ala 640
Val	Leu	Val	Ile	Arg 645	Glu	Lys	Leu	Asp	Ser 650	Ser	Ile	Ala	Ser	Phe 655	Arg
Lys	Lys	Leu	Ala 660	Ile	Arg	Asn	Leu	Glu 665	Pne	Leu	Gln	Val	Ser 670	Gly	Ile
		675	Ile				680	_		_		685			
Val	Lys 690	Val	Asn	Ser	Thr	Lys 695	Lys	Thr	Ile	Arg	Tyr 700	His	Pro	Pro	Glu
Ile 705	Val	Ala	Gly	Leu	Asp 710	Glu	Leu	Ala	Leu	Ala 715	Thr	Glu	His	Leu	Ala 720
Ile	Val	Asn	Arg	Ala 725	Ser	Trp	ązĄ	Ser	Phe 730		Lys	Ser	Phe	Ser 735	Arg
Tyr	Tyr	Thr	Asp 740		Lys	Ala	Ala	Val 745		Ala	Leu	Ala	Ala 750		Asp
Cys	Leu	His 755	Ser	Leu	Ser	Thr	Leu 760		Arg	Asn	Lys	Asn 765		Val	Arg
Pro	Glu 770	Phe	Val	Asp	Asp	Cys 775		Pro	Val	. Glu	780		Ile	Gln	Ser
Gly 785	Arg	His	Pro	Val	Leu 790	Glu	Thr	Ile	Leu	795	_	Asn	Phie	Val	Pro 800
Asn	Asp	Thr	Ile	Leu 805		Ala	Glu	Gly	61u 810		Cys	Gln	Ile	Ile 815	
Gly	Pro	Asn	Met 820	_	Gly	Lys	Ser	Cys	_	: Ile	Arg	Gln	Val 830		Lei

Ile Ser Ile Met Ala Gln Val Gly Ser Phe Val Pro Ala Ser Phe Ala 840 Lys Leu His Val Leu Asp Gly Val Phe Thr Arg Met Gly Ala Ser Asp 855 Ser Ile Gln His Gly Arg Ser Thr Phe Leu Glu Glu Leu Ser Glu Ala 870 875 865 Ser His Ile Ile Arg Thr Cys Ser Ser Arg Ser Leu Val Ile Leu Asp 890 Glu Leu Gly Arg Gly Thr Ser Thr His Asp Gly Val Ala Ile Ala Tyr 905 Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe 920 915 Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly 935 Ser Val Gly Thr Tyr His Val Ser Tyr Leu Thr Leu Gln Lys Asp Lys 955 950 Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg 970 965 Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Gln Leu Ala Gln 985 980 Ile Pro Pro Ser Cys Ile Arg Arg Ala Ile Ser Met Ala Ala Lys Leu Glu Ala Glu Val Arg Ala Arg Glu Arg Asn Thr Arg Met Gly Glu Pro 1015 Glu Gly His Glu Glu Pro Arg Gly Ala Glu Glu Ser Ile Ser Ala Leu 1025 1030

Gly Asp Leu Phe Ala Asp Leu Lys Phe Ala Leu Ser Glu Glu Asp Pro 1045 1050

Trp Lys Ala Phe Glu Phe Leu Lys His Ala Trp Lys Ile Ala Gly Lys 1065

Ile Arg Leu Lys Pro Thr Cys Ser Phe 1075 1080

<210> 20 <211> 24 DNA <212> Artificial sequence <213>

<220>	
<223>	MSH6 specific primer 638 for PCR using cDNA of Arabidopsis
	thaliana ecotype Columbia
<400>	20
-	
tctctaccag g	tgacgaaaa accg 24
<210>	21
<211>	28
<212>	DNA Artificial sequence
<213>	Aftificial sequence
<220>	
<223>	Primer S81 for PCR using cDNA of Arabidopsis thaliana ecotype
	Columbia
<400>	21
cqtcqccttt a	gcatcccct tccttcac 28
J J	
<210>	22
<211>	30 .
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	MSH6 specific primer S823 for PCR using cDNA of Arabidopsis
	thaliana ecotype Columbia
400	
<400>	22
gcttggcgca	totaatagaa toatgacagg 30
210	
<210>	23 24
<211><212>	DNA
	Artificial sequence
<213>	Artificial sequence
<220>	
<223>	MSH6 specific primer 637 for PCR using cDNA of Arabidopsis
	thaliana ecotype Columbia
<400>	23
gacagcgtca	gttcttcaga atgc 24
<210>	24
<211>	33
<212>	DNA

<213>	Artificial sequence	
<220>		
<223>	MSH6 specific primer 1SB for PCR using cDNA of Arabidopsis thaliana ecotype Columbia	s
<400>	24	
atcccgggat	gcagcgccag agatcgattt tgt	33
<210>	25	
<211>	27	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	MSH6 specific primer S83 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia	s
<400>	25	
cgctatctat	ggctgcttcg aattgag	27
<210>	26	
<211>	1385	
<212>	DNA	
<213>	Arabidopsis thaliana ecotype Columbia	
<223>	Clone 43	
<400>	26	
cccgggatgc	agegecagag ategatiting territorice aaaaacecae ggeggegaet	60
acgaagggtt	tggtttccgg cgatgctgct agcggcgggg gcggcagcgg aggaccacga	120
tttaatgtga	aggaagggga tgctaaaggc gacgcttctg tacgttttgc tgtttcgaaa	180
tctgtcgatg	aggttagagg aacggatact ccaccggaga aggttccgcg tcgtgtcctg	240
ccgtctggat	ttaageegge tgaateegee ggtgatgett egteeetgtt etceaatatt	300
atgcataagt	ttgtaaaagt cgatgatcga gattgttctg gagagaggag ccgagaagat	360
gttgttccgc	tgaatgattc atctctatgt atgaaggcta atgatgttat tcctcaattt	120
cgttccaata	atggtaaaac tcaagaaaga aaccatgctt ttagtttcag tgggagagct	480
gaacttagat	cagtagaaga tataggagta gatggcgatg ttcctggtcc agaaacacca	540
gggatgcgtc	cacgtgcttc tcgcttgaag cgagttctgg aggatgaaat gacttttaag	500
gaggataagg	ttcctgtatt ggactctaac aaaaggctga aaatgctcca ggarccggrr	560

tgtggagaga	agaaagaagt	aaacgaagga	accaaatttg	aatggcttga	gtcttctcga	720
atcagggatg	ccaatagaag	acgtcctgat	gatccccttt	acgatagaaa	gaccttacac	780
ataccacctg	atgttttcaa	gaaaatgtct	gcatcacaaa	agcaatattg	gagtgttaag	840
agtgaatata	tggacattgt	gcttttcttt	aaagtgggga	aattttatga	gctgtatgag	900
ctagatgcgg	aattaggtca	caaggagctt	gactggaaga	tgaccatgag	tggtgtggga	950
aaatgcagac	aggttggtat	ctctgaaagt	gggatagatg	aggcagtgca	aaagctatta	1020
gctcgtggat	ataaagttgg	acgaatcgag	cagctagaaa	catctgacca	agcaaaagcc	1080
agaggtgcta	atactataat	tccaaggaag	ctagttcagg	tattaactcc	atcaacagca	1140
agcgagggaa	acatcgggcc	tgatgccgtc	catcttcttg	ctataaaaga	gatcaaaatg	1200
gagctacaaa	agtgttcaac	tgtgtatgga	tttgcttttg	ttgactgtgc	tgccttgagg	1250
ttttgggttg	ggtccatcag	cgatgatçca	tcatgtgctg	ctcttggagc	gttattgatg	1320
caggiticic	caaaggaagt	gttatatgac	agtaaagggc	tatcaagaga	agcacaaaag	1330
gctctaagga	aatatacgtt	gacagggtct	acggcggtac	agttggctcc	agtaccacaa	1440
gtaatggggg	atacagatgc	tgctggagtt	agaaatataa	tagaatctaa	cggatacttt	1500
aaaggttctt	ctgaatcatg	gaactgtgct	gttgatggtc	taaatgaatg	tgatgttgcc	1550
cttagtgctc	ttggagagct	aattaatcat	ctgtctaggc	taaagctaga	agatgtactt	1620
aagcatgggg	atatttttcc	ataccaagtt	tacaggggtt	gtctcagaat	tgatggccag	1580
acgatggtaa	atcttgagat	atttaacaat	agctgtgatg	gtggtccttc	agggaccttg	1740
tacaaatatc	ttgataactg	tgttagtcqa	actggtaagc	gactcttaag	gaattggatc	1800
tgccatccac	tcaaagatgt	agaaagcatc	aataaacggc	ttgatgtagt	tgaagaattc	1860
acggcaaact	cagaaagtat	gcaaatcact	ggccagtatc	tccacaaact	tccagactta	1920
gaaagactgc	teggaegeat	caagtctago	gttcgatcat	cagcctctgt	gttgcctgct	1980
cttctgggga	aaaaagtgct	gaaacaacga	gttaaagcat	ttgggcaaat	tgtgaaaggg	2040
ttcagaagtg	gaattgatct	gttgttggct	ctacagaagg	aatcaaatat	gatgagtttg	2100
ctttataaac	tetgiaaact	tcctatatta	a gtaggaaaaa	gegggetaga	a gttatttctt	2160
tctcaattcg	aadcadccat	agatageg				2188

<210> <211> <212> <213> <223> <400>	27 1385 DNA Arabidops Clone 62	sis chalian	a ecotype Co	olumbia	·	
catcagcctc	tgtgttgcct	gctcttctgg	ggaaaaaagt	gctgaaacaa	cgaqttaaaq	60
	aattgtgaaa					120
aggaatcaaa	tatgatgagt	ttgctttata	aactctgtaa	acttcctata	ttagtaggaa	180
aaagcgggct	agagttattt	ctttctcaat	tcgaagcagc	catagatagc	gactttccaa	240
attatcagaa	ccaagatgtg	acagatgaaa	acgctgaaac	tctcacaata	cttatcgaac	300
tttttatcga	aagagcaact	caatggtctg	aggtcattca	caccataagc	tgcctagatg	360
tcctgagatc	ttttgcaatc	gcagcaagtc	tctctgctgg	aagcatggcc	aggcctgtta	420
tttttcccga	atcagaagct	acagatcaga	atcagaaaac	aaaagggcca	atacttaaaa	480
tccaaggact	atggcatcca	tttgcagttg	cagccgatgg	tcaattgcct	gttccgaatg	540
atatactcct	tggcgaggct	agaagaagca	gtggcagcat	tcatcctcgg	tcattgttac	600
tgacgggacc	aaacatgggc	ggaaaatcaa	ctcttcttcg	tgcaacatgt	ctggccgtta	660
tctttgccca	acttggctgc	tacgtgccgt	gtgagtcttg	cgaaatctcc	ctcgtggata	720
ctatcttcac	aaggcttggc	gcatctgata	gaatcatgac	aggagagagt	acctttttgg	780
tagaatgcac	tgagacagcg	tcagttcttc	agaatgcaac	tcaggattca	ctagtaatcc	840
ttgacgaact	gggcagagga	actagtactt	tcgatggata	cgccattgca	tactcggttt	900
ttcgtcacct	ggtagagaaa	gttcaatgtc	ggatgctctt	tgcaacacat	taccaccctc	960
tcaccaagga	attegegtet	cacccacgtg	tcacctcgaa	acacatggct	tgcgcattca	1020
aatcaagatc	tgattatcaa	ccacgtggtt	gtgatcaaga	cctagtgttc	ttgtaccgtt	1080
taaccgaggg	agcttgtcct	gagagctacg	gacttcaagt	ggcactcatg	gctggaatac	1140
caaaccaagt	ggttgaaaca	gcatcaggtg	ctgctcaagc	catgaagaga	tcaattgggg	1200
aaaacttcaa	gtcaagtgag	ctaagatctg	agttctcaag	tctgcatgaa	gactggctca	1260
agtcattggt	gggtatttct	cgagtcgccc	acaacaatgc	ccccattggc	gaagatgact	1320
acgacacttt	gttttgctta	tggcatgaga	tcaaatcctc	ttactgtgtt	cccaaataac	1380

ccggg	1385
<210>	28
<211>	34
<212>	DNA
<213>	Artificial sequence
(213)	Writing and and
<220>	
<223>	MSH6 specific primer 2S8 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia
<400>	26
atcccgggtt	atttgggaac acagtaagag gatt 34
22.0	
<210>	29
<211>	27
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	MSH6 specific primer S82 for PCR using cDNA of Arabidopsis
(223)	thaliana ecotype Columbia
<400>	29
gcgttcgatc	atcagectet gtgttge 27
<210>	30
<211>	3606
<212>	DNA
<213>	Arabidopsis thaliana ecotype Columbia
	•
<220>	
<221>	CDS
<222>	(142)(3468)
<223>	AtMSH6 full-length cDNA and deduced sequence of the encoded
٠	polypeptide
<400>	30
aaaagttgag	ccctgaggag tatcgtttcc gccatttcta cgacgcaagg cgaaaatttt 60
tggcgccaat	ctttccccc tttcgaattc tctcagctca aaacatcgtt tctctctcac 120
teteteteae	aattccaaaa a atg cag cgc cag aga tcg att ttg tct ttc 171 Met Gln Arg Gln Arg Ser Ile Leu Ser Phe 1 5 10

	ccc Pro									219
	ggc Gly 30									267
	gct Ala						_	_		315
	gag Glu									363
	ctg Leu									411
	ctg Leu									459
	tgt Cys 110									507
	tct Ser									555
	aat Asn			_		_		_		603
	gct Ala								ggc Gly 170	651
	ggt Gly									699
	gtt Val 190									747
	gac Asp									795

tgt Cys	gga Gly 220	gag Glu	aag Lys	aaa Lys	Glu	gta Val 225	aac Asn	gaa Glu	gga Gly	acc Thr	aaa Lys 230	ttt Phe	gaa Glu	tgg Trp	ctt Leu	843
gag Glu 235	tct Ser	cc: Ser	cga Arg	atc Ile	agg Arg 240	gat Asp	gcc Ala	aat Asn	aga Arg	aga Arg 245	cgt Arg	cct Pro	gat Asp	gat Asp	ccc Pro 250	891
ctt Leu	tac Tyr	gat Asp	aga Arg	aag Lys 255	acc Thr	tta Leu	cac His	ata Ile	cca Pro 260	cct Pro	gat Asp	gtt Val	ttc Phe	aag Lys 265	aaa Lys	939
atg Met	tct Ser	gca Ala	tca Ser 270	caa Gln	aag Lys	caa Gln	tat Tyr	tgg Trp 275	agt Ser	gtt Val	aag Lys	agt Ser	gaa Glu 280	tat Tyr	atg Met	987
gac Asp	att Ile	gtg Val 295	ctt Leu	ttc Phe	ttt Phe	aaa Lys	gtg Val 290	GJÀ āāā	aaa Lys	ttt Phe	tat Tyr	gag Glu 295	ctg Leu	tat Tyr	gag Glu	1035
cta Leu	gat Asp 300	gcg Ala	gaa Glu	tta Leu	ggt Gly	cac His 305	aag Lys	gag Glu	ctt Leu	gac Asp	tgg Trp 310	aag Lys	atg Met	acc Thr	atg Met	1083
agt Ser 315	Gly	gtg Val	gga Gly	aaa Lys	tgc Cys 320	aga Arg	cag Gln	gtt Val	ggt Gly	atc Ile 325	Ser	gaa Glu	agt Ser	GJA aaa	ata Ile 330	1131
gat Asp	gag Glu	gca Ala	gtg Val	caa Gln 335	aag Lys	cta Leu	tta Leu	gct Ala	cgt Arg 340	Gly	tat Tyr	aaa Lys	gtt Val	gga Gly 345	cga Arg	1179
atc Ile	gag Glu	cag Gln	cta Leu 350	Glu	aca Thr	tct Ser	gac	caa Gln 355	Ala	aaa Lys	gcc Ala	aga Arg	ggt Gly 360	Ala	aat Asn	1227
act Thr	ata Ile	att Ile 365	Pro	agg Arg	aag Lys	cta Leu	.gtt Val	. Glm	gta Val	tta Leu	act Thr	cca Pro	Ser	aca Thr	gca Ala	1275
ago Sei	gag Glu 380	1 Gl	a aac / Asn	atc lle	ggg ggg	cct Pro	Asp	gco Ala	gto Val	cat His	39(ı Lev	gct Ala	ata Ile	aaa Lys	1323
gag Gl: 39!	ı Ile	aaa Lys	a atg s Met	g gag : Glu	cta Leu 400	Glr	a aag 1 Lys	g tgt s Cys	tca Sei	a act	r Val	g tat l Tyr	gga Gly	ttt Phe	gct Ala 410	1371
tt: Ph	t gti e Val	t gad l Asi	c tgt p Cys	gct s Ala 415	a Ala	ttg Lev	g ago	g tti g Phe	t tgg e Trj 42	o Vai	t ggg	g tco y Sei	ato Ile	ago Ser 42!	c gat r Asp	1419

					gct Ala											1467
aag Lys	gaa Glu	gtg Val 445	tta Leu	tat Tyr	gac Asp	agt Ser	aaa Lys 450	ggg Gly	cta Leu	tca Ser	aga Arg	gaa Glu 455	gca Ala	caa Gln	aag Lys	1515
gct Ala	cta Leu 460	agg Arg	aaa Lys	tat Tyr	acg Thr	ttg Leu 465	aca Thr	ggg	tct Ser	acg Thr	gcg Ala 470	gta Val	cag Gln	ttg Leu	gct Ala	1563
cca Pro 475	gta Val	cca Pro	caa Gln	gta Val	atg Met 480	Gly ggg	gat Asp	aca Thr	gat Asp	gct Ala 485	gct Ala	gga Gly	gtt Val	aga Arg	aat Asn 490	1611
					gga Gly											1659
tgt Cys	gct Ala	gtt Val	gat Asp 510	ggt Gly	ct a Leu	aat Asn	gaa Glu	tgt Cys 515	gat Asp	gtt Val	gcc Ala	ctt Leu	agt Ser 520	gct Ala	Leu	1707
					cat His										ctt Leu	1755
aag Lys	cat His 540	ggg ggg	gat Asp	att Ile	ttt Phe	cca Pro 545	Tyr	caa Gln	gtt Vai	tac Tyr	agg Arg 550	Gly	tgt Cys	ctc Leu	aga Arg	1803
	Asp					Val					Phe				tgt Cys 570	1851
					Gly					Tyr					gtt Val	1899
				Lys					Asn					Pro	ctc Leu	1947
			Glu					Arc					Gli		a ttc ı Phe	1995
		Asr					Glr					n Tyi			c aaa s Lys	2043

ctt Leu 635		-		_	_						aag Lys			_		2091
		-							_		aaa Lys					2139
caa Gln	_	_		-							Gly					2187
	_	_	_	_	-		_	_	_		aat Asn	_				2235
											gga Gly 710					2283
											gat Asp					2331
											gct Ala					2379
Ile	Leu	Ile	Glu 750	Leu	Phe	Ile	Glu	Arg 755	Ala	Thr	caa Gln	Trp	Ser 760	Glu	Val	2427
											tct Ser					2475
												Ile			gaa Glu	2523
						Asn					Gly				aaa Lys 810	2571
					His					Ala					ttg Leu	2619
				Asp					Glu					Ser	ggc	2667

_			cct Pro			-		_	_				_			2715
			ctt Leu													2763
			tac Tyr													2811
			aca Thr									_				2859
			ttg Leu 910													2907
			gat Asp													2955
_			gat Asp					-		_	_		_		_	3003
_			gtt Val		_		_			_						3051
		_	gaa Glu						_	-		_			atg Met	3099
			ttc Phe 990									Arg				3147
	Asp		gtg Val			Tyr					Gly					3195
Ser			ctt Leu		Val					Gly						3243
	Glu		gca Ala	Ser					Ala		Lys			Ile	999 999	3291

Glu Ası	ttc n Phe	Lys					Arg					Ser			3339
gaa gad Glu Asi	Trp		_			Val				-	Val	_			3387
aat gco Asn Ala					Asp	-		_		Leu		_			3435
cat gag His Glu	ı Ile			Ser		-				taaa	tggo	ta			3478
tgacata	aaca (ctato	tgaa	g ct	cgtt	aagt	ctt	ttgo	ctc	téte	gatgt	tt a	attco	tctta	3538
aaaaat	getta	atata	tcaa	a aa	atts	įtit:	c ct	gatt	aaa	aaaa	aaaa	aaa a	aaaa	aaaaa	3598
aaaaaa	aa														3606
<210> <211> <212> <213> <223>	-		: abido	-			na eo	cotyp	oe Co	olumb	oia				
1000		201	.yper) t I de	MS1	16									
<400>		31	.yper	CIGE	· MSF	16									٠
	n Arg	31	-				Ser	Phe 10	Phe	Gln	Lys	Pro	Thr 15	Ala	٠
<400>	_	31 Gln	Arg 5	Ser	Ile	Leu		10					15		
<400> Met Gli	r Thr	31 Gln Lys 20	Arg 5 Gly	Ser	Ile Val	Leu	Gly 25	10 Asp	Ala	Ala	Ser	Gly 30	15 Gly	Gly	
<400> Met Gli 1 Ala Th	r Thr r Gly 35	31 Gln Lys 20 Gly	Arg 5 Gly Pro	Ser Leu Arg	Ile Val Phe	Leu Ser Asn 40	Gly 25 Val	10 Asp Arg	Ala Glu	Ala Gly	Ser Asp 45	Gly 30 Ala	15 Gly Lys	Gly	
<400> Met Gli 1 Ala Thi Gly Sei Asp Ala	r Thr r Gly 35 a Ser	31 Gln Lys 20 Gly Val	Arg 5 Gly Pro	Ser Leu Arg	Ile Val Phe Ala 55	Leu Ser Asn 40 Val	Gly 25 Val Ser	Asp Arg Lys	Ala Glu Ser	Ala Gly Val 60	Ser Asp 45 Asp	Gly 30 Ala Glu	15 Gly Lys Val	Gly Gly Arg	
<400> Met Gli 1 Ala Th: Gly Se: Asp Ala 5 Gly Th:	r Thr r Gly 35 a Ser 0	31 Gln Lys 20 Gly Val	Arg 5 Gly Pro Arg	Ser Leu Arg Phe Pro	Ile Val Phe Ala 55 Glu	Leu Ser Asn 40 Val	Gly 25 Val Ser	Asp Arg Lys	Ala Glu Ser Arg 75	Ala Gly Val 60 Arg	Ser Asp 45 Asp	Gly 30 Ala Glu Leu	15 Gly Lys Val	Gly Gly Arg Ser	
<400> Met Gli 1 Ala Th: Gly Se: Asp Ala 5: Gly Th: 65	r Thr r Gly 35 a Ser 0 r Asp	31 Gln Lys 20 Gly Val Thr	Arg 5 Gly Pro Arg Pro Ala 85	Ser Leu Arg Phe Pro 70 Glu	Ile Val Phe Ala 55 Glu Ser	Leu Ser Asn 40 Val Lys	Gly 25 Val Ser Val	Asp Arg Lys Pro	Ala Glu Ser Arg 75	Ala Gly Val 60 Arg	Ser Asp 45 Asp Val	Gly 30 Ala Glu Leu	15 Gly Lys Val Pro	Gly Gly Arg Ser 80 Ser	

Mec	Lys 130	Ala	Asn	Asp	Val	Ile 135	Pro	Gln	Phe	Arg	Ser 140	Asn	Asn	Gly	Lys
Thr 145	Gln	Glu	Arg	Asn	His 150	Ala	Phe	Ser	Phe	Ser 155	Gly	Arg	Ala	Glu	Leu 160
Arg	Ser	Val	Glu	Asp 165	Ile	Gly	Val	Asp	Gly 170	Asp	Val	Pro	Gly	Pro 175	Glü
Thr	Pro	Gly	Met 180	Arg	Pro	Arg	Ala	Ser 185	Arg	Leu	Lys	Arg	Val 190	Leu	Glu
Asp	Glu	Met 195	Thr	Phe	Lys	Glu	Asp 200	Lys	Val	Pro	Val	Leu 205	Asp	Ser	Asn
Lys	Arg 210	Leu	Lys	Met	Leu	Gln 215	Asp	Pro	Val	Cys	Gly 220	Glu	Lys	Lys	Glu
Val 225	Asn	Glu	Gly	Thr	Lys 230	Phe	Glu	Trp.	Leu	Glu 235	Ser	Ser	Arg	Ile	Arg 240
ąsp	Ala	Asn	Arg	Arg 245	Arg	Pro	Asp	Asp	Pro 250	Leu	Tyr	Asp	Arg	Lys 255	Thr
Leu	His	Ile	Pro 260	Pro	Asp	Val	Phe	Lys 265	Lys	Met	Ser	Ala	Ser 270	Gln	Lys
Gln	Tyr	Trp 275	Ser	Val	Lys	Ser	Glu 280	Tyr	Met	Asp	Ile	Val 285	Leu	Phe	Phe
	290	_				295		_			Asp 300				-
His 305	Lys	Glu	Leu		Trp 310	Lys	Met	Thr	Met	Ser 315	Gly	Val	Gly	Lys	Cys 320
Arg	Gln	Val	Gly	Ile 325	Ser	Glu	Ser	Gly	Ile 330	_	Glu	Ala	Val	Gln 335	-
Leu	Leu	Ala	Arg 340	Gly	Tyr	Lys	Val	Gly 345	_	Ile	Glu	Gln	Leu 350	Glu	Thr
Ser	Asp	Gln 355	Ala	Lys	Ala	Arg	Gly 360	Ala	Asn	Thr	Ile	11e 365		Arg	Lys
Leu	Val 370	Gln	Val	Leu	Thr	Pro 375	Ser	Thr	Ala	Ser	Glu 380	Gly	Asn	Ile	Gly
Pro 385	Asp	Ala	Val	His	Leu 390	Leu	Ala	Ile	Lys	Glu 395	Ile	Lys	Met	Glu	Leu 400
Gln	Lys	Cys	Ser	Thr 405	Val	Tyr	Gly	Phe	Ala 410		Val	Asp	Cys	Ala 415	Ala

Leu	Arg	Phe	Trp 420	Val	Gly	Ser	Ile	Ser 425	Asp	Asp	Ala	Ser	Cys 430	Ala	Ala
Leu	Gly	Ala 435	Leu	Leu	Met	Gln	Val 440	Ser	Pro	Lys	Glu	Val 445	Leu	Tyr	Asp
Ser	Lys 450	Gly	Leu	Ser	Arg	Glu 455	Ala	Gln	Lýs	Ala	Leu 460	Arg	Lys	Tyr	Thr
Leu 465	Thr	Gly	Ser	Thr	Ala 470	Val	Gln	Leu	Ala	Pro 475	Val	Pro	Gln	Val	Met 480
Gly	Asp	Thr	Asp	Ala 485	Ala	Gly	Val	Arg	Asn 490	Ile	Ile	Glu	Ser	Asn 495	Gly
Tyr	Phe	Lys	Gly 500	Ser	Ser	Glu	Ser	Trp 505	Asn	Cys	Ala	Val	Asp 510	Gly	Leu
Asn	Glu	Cys 515	Asp	Val	Ala	Leu	Ser 520	Ala	Leu	Gly	Glu	Leu 525	Ile	Asn	His
Leu	Ser 530	Arg	Leu	Lys	Leu	Glu 535	Asp	Val	Leu	Lys	His 540	Gly	Asp	Ile	Phe
Pro 545	Tyr	Gln	Val	Tyr	Arg 550	Gly	Cys	Leu	Arg	Ile 555	Asp	Gly	Gln	Thr	Met 560
Val	Asn	Leu	Glu	Ile 565	Phe	Asn	Asn	Ser	Cys 570	Asp	Gly	Gly	Pro	Ser 575	Gly
Thr	Leu	Tyr	Lys 580	Tyr	Leu	Asp	Asn	Cys 585	Val	Ser	Pro	Thr	Gly 590	Lys	Arg
Leu	Leu	Arg 595	Asn	Trp	Ile	Cys	His 600	Pro	Leu	Lys	Asp	Val 605	Glu	Ser	Ile
Asn	Lys 610	Arg	Leu	Asp	Val	Val 615	Glu	Glu	Phe	Thr	Ala 620	Asn	Ser	Glu	Ser
Met 625	Gln	Ile	Thr	Gly	Gln 630	Tyr	Leu	His	Lys	Leu 635	Pro	Asp	Leu	Glu	Arg 640
Leu	Leu	Gly	Arg	Ile 645	Lys	Ser	Ser	Val	Arg 650	Ser	Ser	Ala	Ser	Val 655	Leu
Pro	Ala	Leu	Leu 660	Gly	Lys	Lys	Val	Leu 665	Lys	Gln	Arg	Val	Lys 670	Ala	Phe
Gly	Gln	Ile 675	Val	Lys	Gly	Phe	Arg 680	Ser	Gly	Ile	Asp	Leu 685	Leu	Leu	Ala
Leu	Gln 690	Lys	Glu	Ser	Asn	Met 695	Met	Ser	Leu	Leu	Tyr 700	Lys	Leu	Cys	Lys

705	PLO	110	Dea	Val	710	Lys	3-1	Gly	Dea	715	Dea	FIIE	Deu	361	720
Phe	Glu	Ala	Ala	Ile 725	Asp	Ser	Asp	Phe	Pro 730	Asn	Tyr	Gln	Asn	Gln 735	Asp
Val	Thr	Asp	Glu 740	Asn	Ala	Glu	Thr	Leu 745	Thr	Ile	Leu	Ile	Glu 750	Leu	Phe
Ile	Glu	Arg 755	Ala	Thr	Gln	Trp	Ser 760	Glu	Val	Ile	His	Thr 765	Ile	Ser	Cys
Leu	Asp 770	Val	Leu	Arg	Ser-	Phe 775	Ala	Ile	Ala	Ala	Ser 780	Leu	Ser	Ala	Gly
Ser 785	Met	Ala	Arg	Pro	Val 790	Ile	Phe	Pro	Glu	Ser 795	Glu	Ala	Thr	Asp	Gln 800
Asn	Gln	Lys	Thr	Lys 805	Gly	Pro	Ile	Leu	Lys 810	Ile	Gln	Gly	Leu	Trp 815	His
Pro	Phe	Ala	Val 820	Ala	Ala	Asp	Gly	Gln 825	Leu	Pro	Val	Pro	Asn 830	Asp	Ile
Leu	Leu	Gly 835	Glu	Ala	Arg	Arg	Ser 840	Ser	Gly	Ser	Ile	His 845	Pro	Arg	Ser
Leu	Leu 850	Leu	Thr	Gly	Pro	Asn 855	Met	Ģly	Gly	Lys	Ser 860	Thr	Leu	Leu	Arg
Ala 865	Thr	Cys	Leu	Ala	Val 870	Ile	Phe	Ala	Gln	Leu 875	Gly	Cys	Tyr	Val	880
Cys	Glu	Ser	Суѕ	Glu 885		Ser	Leu	Val	Asp 890		Ile	Phe	Thr	Arg 895	Leu
Gly	Ala	Ser	Asp 900	Arg	Ile	Met	Thr	Gly 905	Glu	Ser	Thr	Phe	Leu 910	Val	Glu
Cys	Thr	Glu 915	Thr	Ala	Ser	Val	Leu 920	Gln	Asn	Ala	Thr	Gln 925	Asp	Ser	Lev
Val	Ile 930	Leu	Asp	Glu	Leu	Gly 935	Arg	Gly	Thr	Ser	Thr 940	Phe	Asp	Gly	Туп
Ala 945	Ile	Ala	Tyr	Ser	Val 950	Phe	Arg	His	Leu	Val 955	Glu	Lys	Val	Gln	Cys 960
Arg	Met	Leu	Phe	Ala 965	Thr	His	Tyr	His	Pro 970		Thr	Lys	Glu	Phe 975	
Ser	His	Pro	Arg 980	Val	Thr	Ser	Lys	His 985		Ala	Cys	Ala	Phe 990	-	Se

PCT/EP98/06977

Arg Ser	Asp Ty 995	yr Gln		Gly C 1000	ys Asp	Gln As	p Leu 1005	Val	Pne	Leu		
Tyr Arg 1010	Leu T	hr Glu	Gly Ala 1015	Cys F	ro Glu	Ser Ty 102	r Gly	Leu	Gln	Val		
Ala Leu 1025	Met A		Ile Pro	Asn C	Gln Val	Val Gl 1035	u Thr	Ala	Ser 10	Gly 40	-	
Ala Ala	Gln A	la Met 1045	Lys Arg	Ser 1	lle Gly 1050		n Phe	Lys 1	Ser 1055	Ser		
Glu Leu		er Glu 60	Phe Ser	Ser I	Leu His 065	Glu As	sp Trp	Leu 1070	Lys	Ser		
Leu Val	Gly I 1075	le Ser	Arg Val	Ala 1	His Asn	Asn A	la Pro 1085	Ile	Gly	Glu		
Asp Asp 1090		sp Thr	Leu Phe 1095		Leu Trp	His G	lu Ile 00	Lys	Ser	Ser		
Tyr Cys	Val P	Pro Lys										
			•									
<210>		32										
<211>		24										
<212>		DNA									-	
<213>		Artifi	cial sec	quence						•		
<220>												
<223>			d prime: atellite		PCR am	plifica	tion (of AT	HGEN	ŁA		
<400>		32	-									
accatgo	cata g	cttaaac	tt cttg								-	24
<210>		33										
<211>	·	22										
<212>		DNA			•			•				
<213>		Artifi	cial se	quence	•				•			
<220>	-											
<223>			se prime satellit		PCR am	plifica	tion (of AT	rhge1	IEA		
<400>		33										
acataa	ccac a	aatagg	ggt gc									22

WO 99/19492 PCT/EP98/06977

<210>	34				
<211>	18				
<212>	DNA				
<213>	Artificial sequence				
<220>					
<223>	Forward primer DMCIN-A for PCR	on genomic	DNA	of	Arabidonsis
	thaliana ssp. Landsberg erecta			-	abraoporo
<400>	34				
gaagcgatat	tgttcgtg				. 18
<210>	35				
<211>	18	•			
<212>	DNA .				
<213>	Artificial sequence				•
(213)	Artificial sequence				
<220>					
<223>	Reverse primer DMCIN-B for PCR thaliana ssp. Landsberg erecta		DNA	of	Arabidopsis
<400>	35				
agattgcgag	aacattcc				18
<210>	36				
<211>	31				
<212>	DNA				
<213>	Artificial sequence				
<220>				•	
<223>	Forward primer DMCIN-1 for PCR	on genomic	מזאכו	o €	Arabidoneie
(223)	thaliana ssp. Landsberg erecta		DNA	O1	Arabidopsis
<400>	36				
acgcgtcgac	tcagctatga gattactcgt g				31
<210>	37				
<211>	29				
<212>	DNA				
<213>	Artificial sequence				
<220>					
<223>	Reverse primer DMCIN-2 for PCR	on canomic	אזארן	_ €	Arabidoncis
	thaliana ssp. Landsberg erecta		MM	υĽ	vranigohara
<400>	37				
gctctagatt :	teregeteta agaeratet				29

<210>	38
<211>	32
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer DMCIN-3 for PCR on genomic DNA of Arabidopsis thaliana ssp. Landsberg erecta "Ler"
<400>	38
gctctagaġc t	tctcttaag taagtgattg at 32
<210>	39
<211>	48
<212>	DNA
<213>	Artificial sequence
· <220>	
<223>	Reverse primer DMCIN-4 for PCR on genomic DNA of Arabidopsis thaliana ssp. Landsberg erecta "Ler"
<400>	39
tececeggge t	cgagagate tecatggttt etteagetet atgaatee 48
<210>	40
<211>	26
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer DMCla for PCR on genomic DNA of Arabidopsis thaliana ssp. Landsberg erecta "Ler"
<400>	40
acgcgtcgac g	maattcgcaa gtgggg 26
<210>	41
<211>	38
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer DMClb for PCR on genomic DNA of Arabidopsis
	thaliana ssp. Landsberg erecta "Ler"
<400>	41

tccatggaga	tctcccgggt accgatttgc ttcgaggg 38
<210>	42
<211>	20
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer for PCR amplification of ATEAT1 SSLP marker in Arabidopsis thaliana subspecies
<400>	42
gccactgcgt	gaatgatatg 20
<210>	43
<211>	22
<212>	DNA
<213>	Artificial sequence
(213)	Artificial Sequence
<220>	
<223>	Reverse primer for PCR amplification of ATEAT1 SSLP marker is Arabidopsis thaliana subspecies
<400>	43
cgaacagcca	acattaattc cc 22
<210>	44
<211>	18
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer for PCR amplification of NGA63 SSLP marker in Arabidopsis thaliana subspecies
<400>	44
aaccaaggca	cagaagcg 18
<210>	45
<211>	18
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of NGA63 SSLP marker in Arabidopsis thaliana subspecies

Acccaaging tegecace 18			
210	<400>	45	
210			
210	acccaagiga t	egecace	18
<pre>c2ll> 2l c2ll> DNA c2ll> Artificial sequence c220> c223> Forward primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies c400> 46 taccgaacca aacacaaag g</pre>	4000449094		
<pre>c2ll> 2l c2ll> DNA c2ll> Artificial sequence c220> c223> Forward primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies c400> 46 taccgaacca aacacaaag g</pre>			
<pre>c2ll> 2l c2ll> DNA c2ll> Artificial sequence c220> c223> Forward primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies c400> 46 taccgaacca aacacaaag g</pre>			t
C212> DNA Artificial sequence C220> C223> Forward primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies C400> 46 taccgaacca aaacacaaag g 21 C210> 47 C211> 22 C212> DNA C213> Artificial sequence C220> C223> Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies C400> 47 tctgtatctc ggtgaattct cc 22 C210> 48 C211> 22 C212> DNA C213> Artificial sequence C220> C223> Forward primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies C400> 47 tctgtatctc ggtgaattct cc 22 C210> 48 C211> 22 C212> DNA C213> Artificial sequence C220> C223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies C400> 48 ggtctgttga tgtcgtaagt cg 22 C210> 49 C211> 22 C212> DNA C213> Artificial sequence			
<pre><213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies <400> 46 taccgaacca aaacacaaag g 21 <210> 47</pre>			
<pre><220> <223> Forward primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies <400> 46 taccgaacca aaacacaaag g</pre>	<212>	DNA .	
Porward primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies 400> 46 taccgaacca aaacacaaag g 21 <210> 47	<213>	Artificial sequence	
Porward primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies 400> 46 taccgaacca aaacacaaag g 21 <210> 47			
Porward primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies 400> 46 taccgaacca aaacacaaag g 21 <210> 47	<220>		
Arabidopsis thaliana subspecies <400> 46 taccgaacca aacacaaag g 21 <210> 47 <211> 22 <212> DNA <213> Artificial sequence <220> 4223> Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies <400> 47 tctgtatctc ggtgaattct cc 22 <211> DNA <211> 22 <212> DNA <221> Artificial sequence <220 <400> 47 tctgtatctc ggtgaattct cc 22 <221> DNA <213> Artificial sequence <220> 4212> DNA <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 49 <211> 22 <212> DNA <213> Artificial sequence <2210 49 <221> 22 <212> DNA <213> Artificial sequence <2210 49 <2211 22 <212> DNA <213> Artificial sequence		Forward primer for DCP amplification of NGA248	SSID marker in
<pre>c400> 46 taccgaacca aaacacaaag g 21 c210> 47 c211> 22 c212> DNA c213> Artificial sequence c220> c223> Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies c400> 47 tctgtatctc ggtgaattct cc 22 c212> DNA c213> Artificial sequence c210> 48 c211> 22 c212> DNA c213> Artificial sequence c220> c223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies c400> 48 ggtctgttga tgtcgtaagt cg 22 c210> 48 ggtctgttga tgtcgtaagt cg 22 c210> 49 c211> 22 c212> DNA c213> Artificial sequence</pre>	(2237		SSBF Marker III
taccgaacca aaacacaaag g 21 <210> 47 <211> 22 <212> DNA <213> Artificial sequence <220> <223> Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies <400> 47 tctgtatctc ggtgaattct cc 22 <210> 48 <211> 22 <212> DNA <213> Artificial sequence <220> <220> <220> 222> Eoward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 48 ggtctgttga tgtcgtaagt cg 22 <210> Ag <210 A		Arabidopsis challana subspecies	
taccgaacca aaacacaaag g 21 <210> 47 <211> 22 <212> DNA <213> Artificial sequence <220> <223> Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies <400> 47 tctgtatctc ggtgaattct cc 22 <210> 48 <211> 22 <212> DNA <213> Artificial sequence <220> <220> <220> 222> Eoward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 48 ggtctgttga tgtcgtaagt cg 22 <210> Ag <210 A			
<pre> c210> 47 c211> 22 c212> DNA c213> Artificial sequence c220> c223> Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies c400> 47 tctgtatctc ggtgaattct cc</pre>	<400>	46	
<pre> c210> 47 c211> 22 c212> DNA c213> Artificial sequence c220> c223> Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies c400> 47 tctgtatctc ggtgaattct cc</pre>		·	
<pre> <210> 47 <211> 22 <212> DNA <213> Artificial sequence <220> <223> Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies <400> 47 tctgtatctc ggtgaattct cc</pre>	taccgaacca a	aaacacaaag g	21
<pre><211> 22 <212> DNA <213> Artificial sequence </pre> <pre><220> <223> Reverse primer for PCR amplification of NGA248 SSLP marker in</pre>	-		
<pre><211> 22 <212> DNA <213> Artificial sequence </pre> <pre><220> <223> Reverse primer for PCR amplification of NGA248 SSLP marker in</pre>			
<pre><211> 22 <212> DNA <213> Artificial sequence </pre> <pre><220> <223> Reverse primer for PCR amplification of NGA248 SSLP marker in</pre>	~210×	47	•
<pre> c212> DNA c213> Artificial sequence c220> c223> Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies c400> 47 tctgtatctc ggtgaattct cc 22 c210> 48 c211> 22 c212> DNA c213> Artificial sequence c220> c223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies c400> 48 ggtctgttga tgtcgtaagt cg 22 c210> 49 c211> 22 c212> DNA c213> Artificial sequence c210> 49 c211> 22 c212> DNA c213> Artificial sequence c210> Ag c211> 22 c212> DNA c213> Artificial sequence c210> A</pre>			
<pre> <213> Artificial sequence <220> <221> Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies <400> 47 tctgtatctc ggtgaattct cc 22 <210> 48 <211> 22 <212> DNA <213> Artificial sequence <220> <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 49 <211> 22 <212> DNA <213> Artificial sequence <220> <210> AR </pre>			
<pre> <220> <223> Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies <400> 47 tctgtatctc ggtgaattct cc 22 <210> 48 <211> 22 <212> DNA <213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 49 <211> 22 <212> DNA <213> Artificial sequence <220> AB </pre>			
Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies 400> 47 tctgtatctc ggtgaattct cc 22 210> 48 221> 20, 212> DNA 213> Artificial sequence 220> 223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies 400> 48 ggtctgttga tgtcgtaagt cg 22 210> 49 221> DNA Artificial sequence 220 ARTIFICIAL SSLP marker in Arabidopsis thaliana subspecies	<213>	Artificial sequence	
Reverse primer for PCR amplification of NGA248 SSLP marker in Arabidopsis thaliana subspecies 400> 47 tctgtatctc ggtgaattct cc 22 210> 48 221> 20, 212> DNA 213> Artificial sequence 220> 223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies 400> 48 ggtctgttga tgtcgtaagt cg 22 210> 49 221> DNA Artificial sequence 220 ARTIFICIAL SSLP marker in Arabidopsis thaliana subspecies			
Arabidopsis thaliana subspecies <400> 47 tctgtatctc ggtgaattct cc 22 <210> 48 <221> 22 <212> DNA <213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 49 <211> 22 <212> DNA Artificial sequence	<220>		
Arabidopsis thaliana subspecies <400> 47 tctgtatctc ggtgaattct cc 22 <210> 48 <221> 22 <212> DNA <213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 49 <211> 22 <212> DNA Artificial sequence	<223>	Reverse primer for PCR amplification of NGA248	S SSLP marker in
<pre></pre>			
<pre>cctgtatctc ggtgaattct cc <210> 48 <211> 22 <212> DNA <213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg</pre>		•	
<pre>cctgtatctc ggtgaattct cc <210> 48 <211> 22 <212> DNA <213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg</pre>	<400>	47	
<pre> <210> 48 <211> 22 <212> DNA <213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg</pre>	1100>		
<pre> <210> 48 <211> 22 <212> DNA <213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg</pre>			22
<pre> <211> 22 <212> DNA <213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 49 <211> 22 <212> DNA <213> Artificial sequence</pre>	teligratere s	gyeyaacce ee	22
<pre> <211> 22 <212> DNA <213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 49 <211> 22 <212> DNA <213> Artificial sequence</pre>			
<pre> <211> 22 <212> DNA <213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 49 <211> 22 <212> DNA <213> Artificial sequence</pre>			
<pre> <212> DNA <213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg</pre>	<210>	48	
<pre> <213> Artificial sequence <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 49 <211> 22 <212> DNA <213> Artificial sequence</pre>	<211>	22	
<pre> <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 49 <211> 22 <212> DNA <213> Artificial sequence</pre>	<212>	DNA -	
<pre> <220> <223> Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 49 <211> 22 <212> DNA <213> Artificial sequence</pre>	<213>	Artificial sequence	•
Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies 400> 48 ggtctgttga tgtcgtaagt cg 22 210> 49 221> 22 212> DNA Artificial sequence		· ·	
Forward primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies 400> 48 ggtctgttga tgtcgtaagt cg 22 210> 49 221> 22 212> DNA Artificial sequence	c2205	·	
Arabidopsis thaliana subspecies <400> 48 ggtctgttga tgtcgtaagt cg 22 <210> 49 <211> 22 <212> DNA <213> Artificial sequence		Forward primer for DCP amplification of NCA131	CCID marker in
<pre><400> 48 ggtctgttga tgtcgtaagt cg</pre>	(223)		33DF Marker III
<pre>ggtctgttga tgtcgtaagt cg <210> 49 <211> 22 <212> DNA <213> Artificial sequence</pre>		Arabidopsis thallana subspecies	
<pre>ggtctgttga tgtcgtaagt cg <210> 49 <211> 22 <212> DNA <213> Artificial sequence</pre>			
<210> 49 <211> 22 <212> DNA <213> Artificial sequence	<400>	48	
<210> 49 <211> 22 <212> DNA <213> Artificial sequence			
<210> 49 <211> 22 <212> DNA <213> Artificial sequence	ggtctgttga	tgtcgtaagt cg	22
<211> 22 <212> DNA <213> Artificial sequence			
<211> 22 <212> DNA <213> Artificial sequence			
<211> 22 <212> DNA <213> Artificial sequence	c210s	49	
<212> DNA <213> Artificial sequence			
<213> Artificial sequence			
			<i>'</i>
<220>	<213>	Artificial sequence	
<220>			
	<220>		

WO 99/19492 PCT/EP98/06977

<223>	Reverse primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies
<400>	49
atcttgaaac c	tttagggag gg 22
<210>	50
<211>	22
<212>	DNA
<213>	Artificial sequence
	•
<220>	
<223>	Forward primer for PCR amplification of NGA280 SSLP marker in Arabidopsis thaliana subspecies
<400>	50
ctgatctcac g	gacaatagt gc 22
<210>	51
<211>	20
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of NGA280 SSLP marker in Arabidopsis thaliana subspecies
<400>	51
ggctccataa aa	aagtgcacc 20
<210>	52
<211>	21
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primar for BCB amplification of Montage control in
	Forward primer for PCR amplification of NGA111 SSLP marker in Arabidopsis thaliana subspecies
<400>	52
ctccagttgg aa	agctaaagg g 21
-210	
<210>	53
<211>	21
<212>	DNA
<213>	Artificial sequence

<220>			-		
<223>	Reverse primer for PCR amplification of Arabidopsis thaliana subspecies	NGA111	SSLP	marker	in
<400>	53				
tgttttttag g	acaaatggc g				21
	•				
<210>	54				
<211>	20				
<212>	DNA	•			
<213>	Artificial sequence				
<220>					
<223>	Forward primer for PCR amplification of Arabidopsis thaliana subspecies	NGA168	SSLP	marker	in
<400>	5 4				
ccttcacatc c	aaaacccac				20
<210>	55			•	
<211>	20				
<212>	DNA			•	
<213>	Artificial sequence				
<220>					
<223>	Reverse primer for PCR amplification of Arabidopsis thaliana subspecies	NGA168	SSLP	marker	in
<400>	55				
gcacataccc a	caaccagaa				20
	-				
<210>	56				
<211>	20				
<212>	DNA			•	
<213>	Artificial sequence				
<220>					
<223>	Forward primer for PCR amplification of in Arabidopsis thaliana subspecies	NGA112	S SSL	P marke:	r
<400>	56				

cgctacgctt ttcggtaaag

<210>	57 ·
<211>	20
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of NGA1126 SSLP marker
	in Arabidopsis thaliana subspecies
<400>	57
gcacagtcca	agtcacaacc
· ·	20
<210>	58
<211>	20
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer for PCR amplification of NGA361 SSLP marker in
	Arabidopsis thaliana subspecies
	on and the point of the state o
<400>	58
aaagagatga	gaatttggac 20
	20
<210>	59
<211>	23
<212>	DNA
<213>	Artificial sequence
<220>	•
<223>	Reverse primer for PCR amplification of NGA361 SSLP marker in
	Arabidopsis thaliana subspecies
	• • • • • • • • • • • • • • • • • • • •
<400>	59
acatatcaat a	atattaaagt agc 23
•	
<210>	60
<211>	18
<212>	DNA
<213>	Artificial sequence
	-
<220>	
<223>	Forward primer for PCR amplification of NGA168 SSLP marker in
	Arabidopsis thaliana subspecies
-400-	

tegtetactg	cactgccg
<210>	61
<211>	22
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of NGA168 SSLP marker in Arabidopsis thaliana subspecies
<400>	61
gaggacatgt	ataggagcct cg 22
•	
<210>	62
<211>	20
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer for PCR amplification of AthBIO2 SSLP marker
(223)	in Arabidopsis thaliana subspecies
<400>	62
tgacctcctc	ttccatggag 20
<210>	63 [°]
<211>	22
<212>	DNA
<213>	Artificial sequence
<220>	The state of the s
<223>	Reverse primer for PCR amplification of AthBIO2 SSLP marker in Arabidopsis thaliana subspecies
<400>	63
ttaacagaaa	cccaaagctt tc 22
<210>	64
<211>	21
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer for PCR amplification of AthUBIQUE SSLP marke in Arabidopsis thaliana subspecies

<400>	64
aggcaaatgt	ccatttcatt g
<210>	65
<211>	20
<212>	DNA
<213>	Artificial sequence
; <220>	
<223>	Reverse primer for PCR amplification of AthUBIQUE SSLP marker in Arabidopsis thaliana subspecies
<400>	65
acgacatggc	agatttctcc 20
<210>	66
<211>	21
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer for PCR amplification of NGA172 SSLP marker in
	Arabidopsis thaliana subspecies
<400>	66
agctgcttcc	ttatagcgtc c 21
<210>	67
<211>	19
<212>	DNA
<213>	Artificial sequence
	· · · · · · · · · · · · · · · · · · ·
<220>	
<223>	Reverse primer for PCR amplification of NGA172 SSLP marker in Arabidopsis thaliana subspecies
<400>	67
catecgaatg o	ccattgttc 19
<210>	68
<211>	21
<212>	DNA
<213>	Artificial sequence
<220>	

<223>	Forward primer for PCR amplification of NGA126 SSLP marker in Arabidopsis thaliana subspecies
<400>	53
gaaaaaacgc t	actttcgtg g 21
<210>	69
<211>	22
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of NGA126 SSLP marker in Arabidopsis thaliana subspecies
<400>	69
caagagcaat a	tcaagagca gc 22
210	
<210>	70
<211>	20
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer for PCR amplification of NGA162 SSLP marker in
	Arabidopsis thaliana subspecies
. 4.00	70
<400>	70
catgcaattt g	catctgagg 20
<210>	71
<211>	22
<212>	DNA
<213>	Artificial sequence
(213)	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of NGA162 SSLP marker in
	Arabidopsis thaliana subspecies
<400>	71
ctctgtcact c	ttttcctct gg 22
<210>	72
<211>	21
<212>	DNA
<213>	Artificial sequence
	···· ··· ··· ··· ··· ··· ··· ··· ··· ·

<220>				•		
<223>	Forward primer for PCR amplification Arabidopsis thaliana subspecies	of	NGA6	SSLP	marker	in
<400>	72					
tggatttctt	cctctcttca c					21
<210>	73					
<211>	21					
<212>	DNA					
<213>	Artificial sequence					
<220>						
<223>	Reverse primer for PCR amplification Arabidopsis thaliana subspecies	of	NGA6	SSLP	marker	in
<400>	73				-	
atggagaagc	ttacactgat ć					21
<210>	74					
<211>	20					
<212>	DNA					
<213>	Artificial sequence					
<220>						
<223>	Forward primer for PCR amplification Arabidopsis thaliana subspecies	of	NGA1	2 SSL	P markeı	in
<400>	74					
aatgttgtcc	tcccetcctc					20
<210>	75					
<211>	22				•	
<212>	DNA					
<213>	Artificial sequence					
<220>						
<223>	Reverse primer for PCR amplification Arabidopsis thaliana subspecies	of	NGA1	2 SSL	P marker	in
<400>	75					
tgatgctctc	tgaaacaaga gc					22

<210>	76	
<211>	21	
<212>	DNA	
<213>	Artificial sequence	
<220>	•	
<223>	Forward primer for PCR amplification of NGA8 SSLP marker i Arabidopsis thaliana subspecies	n
<400>	76	
gagggcaaat	ctttatttcg g	21
<210>	77	
<211>	22	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Reverse primer for PCR amplification of NGA8 SSLP marker i Arabidopsis thaliana subspecies	n
<400>	77	
tggctttcgt	ttataaacat cc	22
<210>	78	
<211>	21	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Forward primer for PCR amplification of NGA1107 SSLP marke in Arabidopsis thaliana subspecies	r
<400>	7,8	
gcgaaaaaac	aaaaaaatcc a	21
· <210>	79	
<211>	21	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Reverse primer for PCR amplification of NGA1107 SSLP marked in Arabidopsis thaliana subspecies	r
400		

cgacgaatcg	acagaattag g	-	21
<210>	80		
<211>	21		
<212>	DNA		
<213>	Artificial sequence		
<220>			
<223>	Forward primer for PCR amplification of NGA225 Arabidopsis thaliana subspecies	SSLP marker	in
<400>	80		
gaaatccaaa (tcccagagag g		21
<210>	81		
<211>	22		
<212>	DNA		
<213>	Artificial sequence		
<220>			
<223'>	Reverse primer for PCR amplification of NGA225 Arabidopsis thaliana subspecies	SSLP marker	in
<400>	81		
tctccccact a	ägttttgtgt cc		22
<210>	82		
<211>	19		
<212>	DNA		
<213>	Artificial sequence		
<220>			
<223>	Forward primer for PCR amplification of NGA249 Arabidopsis thaliana subspecies	SSLP marker	in
<400>	82		
taccgtcaat t	tcatcgcc		19
-210 -			
<210> <211>	83		
<211> <212>	22		
<212>	DNA Artificial sequence		
<220>			
<223>	Reverse primer for PCR amplification of NGA249 stabidopsis thaliana subspecies	SSLP marker	in

46

<400>	83
ggatccctaa c	tgtaaaatc cc 22
<210>	84
<211>	22
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer for PCR amplification of CA72 SSLP marker in Arabidopsis thaliana subspecies
<400>	84
aatcccagta a	ccaaacaca ca 22
<210>	85
<211>	20
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of CA72 SSLP marker in Arabidopsis thaliana subspecies
<400>	85
cccagtctaa c	cacgaccac 20
<210>	86
<211>	20
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer for PCR amplification of NGA151 SSLP marker in Arabidopsis thaliana subspecies
<400>	86
gttttgggaa g	ttttgctgg 20-
geeregggaa g	20
<210>	87
<211>	24
<212>	DNA
<213>	Artificial sequence
<220>	

<223>	Reverse primer for PCR amplification of NGA151 SSLP marker in Arabidopsis thaliana subspecies
<400>	87
cagtctaaaa g	gcgagagtat gatg 24
<210>	88
<211>	22
	DNA
<213>	Artificial sequence
10137	Arciriciai bequence
<220>	
<223>	Forward primer for PCR amplification of NGA106 SSLP marker in
	Arabidopsis thaliana subspecies
<400>	88
gttatggagt :	tctagggca cg
3000033030	cccagggca cg . 22
<210>	89
<211>	20
<212>	DNA
<213>	Artificial sequence
	•
<220>	
<223>	Reverse primer for PCR amplification of NGA106 SSLP marker in
	Arabidopsis thaliana subspecies
<400>	89
tgccccattt t	GEFGFFG
cycocaccc c	20
<210>	90
<211>	20.
<212>	DNA
<213>	Artificial sequence
<220>	•
<223>	Forward primer for PCR amplification of NGA139 SSLP marker in
	Arabidopsis thaliana subspecies
<400>	90
30300F3663 @	
agagctacca g	atccgatgg 20
<210>	91
<211>	21
<212>	DNA
<213>	Artificial sequence

<220>						
<223>	Reverse primer for PCR amplification of Arabidopsis thaliana subspecies	of	NGA139	SSLP	marke	er i
<400>	91					
ggtttcgttt	cactatccag g					21
	• -					
<210>	92					
<211>	22					
<212>	DNA					
<213>	Artificial sequence					
<220>	•					
<223>	Forward primer for PCR amplification of Arabidopsis thaliana subspecies	of	NGA76	SSLP	markeı	in
<400>	92					
ggagaaaatg	tcactctcca cc					22
<210>	93					
<211>	20					
<211>	DNA					
<213>	Artificial sequence					
(213)	Altilitial sequence					
<220>						
<223>	Reverse primer for PCR amplification of Arabidopsis thaliana subspecies	of	NGA76	SSLP	marke	r in
<400>	93					
aggcatggga	gacatttacg					20
<210>	94					
<211>	20					
<212>	DNA					
<213>	Artificial sequence					
(213)	Altificial sequence					
<220>	·					
<223>	Forward primer for PCR amplification of in Arabidopsis thaliana subspecies	of	ATHSO1	.91 SS	SLP ma:	rker
<400>	94					
ctccaccaat	catgcaaatg					20

<210>	95	
<211>	21	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Reverse primer for PCR amplification of ATHSO191 SSLP mark in Arabidopsis thaliana subspecies	cer
<400>	95	
tgatgttga	t ggagatggtc a	21
<210>	96	
<211>	22	
<212>	DNA	
<213>	Artificial sequence	
(213)	Artificial sequence	
<220>		
<223>	Forward primer for PCR amplification of NGA129 SSLP marker Arabidopsis thaliana subspecies	: iı
<400>	96	
tcaggagga	a ctaaagtgag gg	22
<210>	97	
<211>	22	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Reverse primer for PCR amplification of NGA129 SSLP marker Arabidopsis thaliana subspecies	ir
<400>	97	
cacactgaag	g atggtcttga gg	22
<210>	98	
<211>	8062	
<212>	DNA	
<213>	Arabidopsis thaliana ecotype Columbia	
<220>		
<223>	Genomic DNA sequence of AtMSH6	
<400>	97	
ttttttggtt	gctaacaata aaggtatacg gttttatgtc atcaatataa ctatataa	60

aayaaatyaa	agatatatat	rgtttttta	cccaccaaac	aaaacaacaa	gactttttt	120
ttacttttta	cattggtcaa	caaaatacaa	gataaacgac	atcgtttaat	catttcccaa	180
tttacccct	aagtttaaca	cctagaacct	tctccatctt	cgcaagcaca	gcctgattag	240
gaacagcttt	accattctca	tattcctgaa	ctacctgagt	cctctcattg	atctgtttcg	300
ccaaatccgc	ttgtgacatc	ttcttctcca	atctcgcttt	ctgtatcatc	aacctcacct	360
ctgctttcac	acgatccatc	gccgcaggct	ctgtttcttc	ttccagcttc	ttcgtgttaa	420
tcaccggaac	cgccgtagat	ttcccctttt	tgttcgaacc	ggcatcgaat	ttcttaaccg	480
tttgaaccgc	gacaccgttt	ctcagagctg	cgttaaccgc	tttcggatcg	cgtaggtctt	540
gctcttttg	ttttgatttg	tggagaacta	ctggttccca	gtcttgtgtt	actgctcctg	600
ggtatctgct	cggcatcgtc	gatgaattga	gagaaaggaa	caacgcgaaa	attttattaa	660
tctgagtttt	gaaattgaga	aacgatgaag	atgaagaatg	ttgttgagag	gattgtgata	720
tttatatata	cgaagattgg	tttctggaga	attcgatcat	cttttctcc	attttcgtct	780
ctggaacgtt	cttagagatg	attgacgacg	tgtcattatc	tgatttgcag	ttaaccaatg	840
ctttttgggt	tggattcgtg	gtacaccata	ttatccgatt	tggctcaatg	gttttatata	900
aatttggttt	tcggttcggt	tatgagttat	cattaaaatt	aagctaacca	aaaattttcg	960
taaaatttat	ttcggtttca	attcggatcc	cttacttcca	gaaccgaatt	attcgaaacc	1020
ggggttagcc	gaaccgaata	ccaatgcctg	attgactcgt	tggctagaaa	gatccaacgg	1080
tatacaataa	tagaacataa	atcggacggt	catcaaagcc	tcaaagagtg	aacagtcaac	1140
aaaaaagtt	gagecetgag	gagtatcgtt	teegecattt	ctacgacgca	aggcgaaaat	1200
ttttggcgcc	aatctttccc	ccctttcgaa	ttctctcagc	tcaaaacatc	gtttctctct	1260
cactetetet	cacaattcca	aaaaatgcag	cgccagagat	cgattttgtc	tttcttccaa	1320
aaacccacgg	cggcgactac	gaagggtttg	gtttccggcg	atgctgctag	cggcgggggc	1380
ggcagcggag	accacgattt	aatgtgaagg	aaggggatgc	taaaggcgac	gcttctgtac	1440
gttttgctgt	ttcgaaatct	gtcgatgagg	ttagaggaac	ggatactcca	ccggagaagg	1500
ttccgcgtcg	tgtcctgccg	tctggattta	agccggctga	atccgccggt	gatgcttcgt	1560
ccctgttctc	caatattatg	cataagtttg	taaaagtcga	tgatcgagat	tgttctggag	1620
agaggtacta	atcttcgatt	CECEFAREE	tatrarett	200000000000000000000000000000000000000	agaagattcg	1680

tgtaatttgt	Egrattegtt	ggagagattc	tgattattge	attggatcgt	tgtttacaaa	1/40
ttttcaggag	ccgagaagat	gttgttccgc	tgaatgattc	atctctatgt	atgaaggcta	1800
atgatgttat	tcctcaattt	cgttccaata	atggtaaaac	tcaagaaaga	aaccatgctt	1860
ttagtttcag	tgggagagct	gaacttagat	cagtagaaga	tataggagta	gatggcgatg	1920
ttcctggtcc	agaaacacca	gggatgcgtc	cacgtgcttc	tcgcttgaag	cgagttctgg	1980
aggatgaaat	gacttttaag	gaggataagg	ttcctgtatt	ggactctaac	aaaaggctga	2040
aaatgctcca	ggatccggtt	tgtggagaga	agaaagaagt	aaacgaagga	accaaatttg	2100
aatggcttga	gtcttctcga	atcagggatg	ccaatagaag	acgtcctgat	gateceettt	2160
acgatagaaa	gaccttacac	ataccacctg	atgttttcaa	gaaaatgtct	gcatcacaaa	2220
agcaatattg	gagtgttaag	agtgaatata	tggacattgt	gcttttcttt	aaagtggtta	2280
gtaactatta	atctagtgtt	caatccattt	cctcaatgtg	atttgttcac	ttacatctgt	2340
ttacgttatg	ctcttctcag	gggaaatttt	atgagctgta	tgagctagat	gcggaattag	2400
gtcacaagga	gcttgactgg	aagatgacca	tgagtggtgt	gggaaaatgc	agacaggtaa	2460
attagttgaa	acaactggcc	tgcttgaatt	attgtgtcta	taaattttga	caccaccttt	2520
tgtttcaggt	tggtatctct	gaaagtggga	tagatgaggc	agtgcaaaag	ctattagctc	2580
gtgggtaagg	gaaccatcat	actttatgga	attcgtttac	tgctacttcg	gctaggattt	2640
aagaaatgga	aatcacttca	agcatcatta	gttaggatcc	tgagaactca	ggatgttttc	2700
ttattcgtta	tataataagt	cttttcatca	aggagtaaca	aacaaaactt	gcacaatatt	2760
tgtgtgctca	ctggcaaggc	atatataccc	agctaacctt	tgctagttca	ctgtagtaac	2820
agttacggat	aatatatgtt	tacttgtatg	tggtaccctc	attttgtctc	tcatggaggc	2880
tttcaagcct	tgtgttgaaa	ctggatagtt	acatatgctt	ccaacagaaa	ctagcatgca	2940
gattcatatg	ctttcctatt	ctactaatta	tgtattgaca	cactcgttgt	ttcttttgaa	3000
agatataaag	ttggacgaat	cgagcagcta	gaaacatctg	accaagcaaa	agccagaggt	3060
gctaatactg	taagttttct	tggataggtc	aaggagagtg	ttgcagactg	tttttgatca	3120
tttcttttc	tgtacattac	tttcatgctg	taattaactc	aatggctatt	ctggtctgat	3180
tatcagataa	ttccaaggaa	gctagttcag	gtattaactc	catcaacagc	aagcgaggga	3240
aacatcgggc	ctgatgggg	ccatcrtctt	actataaaaa	acceptate	tttacttatt	3300

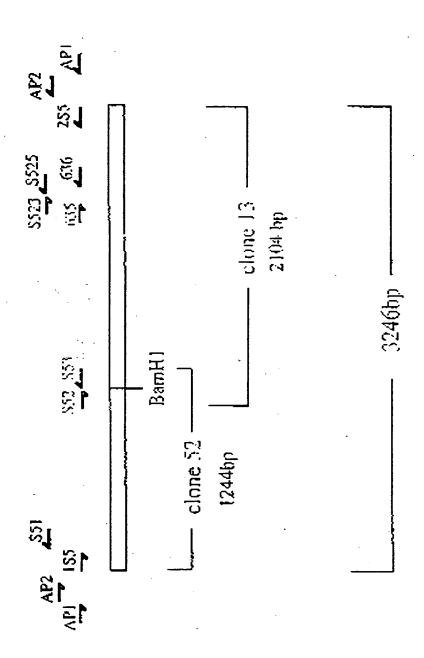
tatcttatca	tgttcagttc	atccaagtcc	tgaaaaatta	cactcttctt	taccaatctt	3360
ccatcaagct	gtgtaaagga	tttggaatta	gaaaatcatt	atttgatgct	ttgttttata	3420
tgcaagaggt	tcccttgaaa	agatctgttt	aagattcttt	gcacttgaaa	aattcaatct	3480
ttttaagtga	atcccctact	ttcttacaat	gatcatagtc	tgcaattgca	tgtcaagtaa	3540
tatcattcct	tgttactgca	tccccctctt	tcttaatgac	cattgtctat	gttgtgtttg	3600
tctcgtgtgc	tggagaaaat	gatagctgat	ccaagctgta	cattatcatg	attaagtagc	3660
tgctcaggaa	ttgcctttgg	ttacattgcc	taatggtttg	atgtcaattt	ttcttctgaa	3720
tctttattt	agatcaaaat	ggagctacaa	aagtgttcaa	ctgtgtatgg	atttgctttt	3780
gttgactgtg	ctgccttgag	gttttgggtt	gggtccatca	gcgatgatgc	atcatgtgct	3840
gctcttggag	cgttattgat	gcaggtaagc	aagtgtattc	tgtatcttat	gtgtaccatg	3900
tgacttcctg	tgcatatatt	tgggttgcag	gaactaattc	tgaatcacca	tttggtatgt	3960
ttttccagg	tttctccaaa	ggaagtgtta	tatgacagta	aaggtaaact	gcttgtatcg	4020
ccagttgttt	tgttaaacag	aatttaaggt	aaatgacact	ggttaattta	aagtgcatac	4080
atgttgaaat	attgcagggc	tatcaagaga	agcacaaaag	gctctaagga	aatatacgtt	4140
gacaggtacc	atttcagtag	gcaagctaac	tgacaattta	accgctcacc	gaatgatagg	4200
tctcttaaac	attgctaatg	tagatgatgt	ttatgtttca	atctaatagg	gtctacggcg	4260
gtacagttgg	ctccagtacc	acaagtaatg	ggggatacag	atgctgctgg	agttagaaat	4320
ataatagaat	ctaacggata	ctttaaaggt	tcttctgaat	catggaactg	tgctgttgat	4380
ggtctaaatg	aatgtgatgt	tgcccttagt	gctcttggag	agctaattaa	tcatctgtct	4440
aggctaaagg	tgtgttggct	tgtttagttt	ttgcttttca	caaattaagc	aaaggaactt	4500
ttcataactt	acagtttcta	tctacttgca	gctagaagat	gtacttaagc	atggggatat	4560
ttttccatac	caagtttaca	ggggttgtct	cagaattgat	ggccagacga	tggtaaatct	4620
tgagatattt	aacaatagct	gtgatggtgg	tccttcaggc	aagtgcatat	ttcttttttg	4680
ataacttcaa	ctagagggca	gacatagaag	gaaaaattct	aatacttcgt	acggatctcc	4740
agtaagtaat	agccgatttt	tgtttaccta	tgtagggacc	ttgtacaaat	atcttgataa	4800
ctgtgttagt	ccaactggta	agcgactctt	aaggaattgg	atctgccatc	cactcaaaga	4860
tgtagaaagc	atcaataaac	ggcttgatgt	agttgaagaa	ttcacggcaa	actcagaaag	4920

catgedaate	accygecage	atctccacaa	acttccagac	ttagaaagac	tgctcggacg	4980
catcaagtct	agcgttcgat	catcagcctc	tgtgttgcct	gctcttctgg	ggaaaaaagt	5040
gctgaaacaa	cgagtaagta	tcaatcacaa	gttttctgag	taatgccttc	catgagtagt	5100
ataggactaa	aacattacgg	gtctagctaa	agactgttct	ccttcttttg	caatgtctgg	5160
ttattcatta	catttctctt	aacttattgc	attgcaggtt	aaagcatttg	ggcaaattgt	5220
gaaagggttc	agaagtggaa	ttgatctgtt	gttggctcta	cagaaggaat	caaatatgat	5280
gagtttgctt	tataaactct	gtaaacttcc	tatattagta	ggaaaaagcg	ggctagagtt	5340
atttctttct	caattcgaag	cagccataga	tagcgacttt	ccaaattatc	aggtgcccat	5400
ctatctttca	tactttacaa	caaaatgtct	gtcactactc	aaagcaatgc	atatggctta	5460
gatctcaact	cacaccccga	ggatcctaaa	gggatttgct	ttttattcct	aatgtttttg	5520
gatggtttga	tttatttcta	acttgaactt	attaatcttg	taccagaacc	aagatgtgac	5580
agatgaaaac	gctgaaactc	tcacaatact	tatcgaactt	tttatcgaaa	gagcaactca	5640
atggtctgag	gtcattcaca	ccataagctg	cctagatgtc	ctgagatctt	ttgcaatcgc	5700
agcaagtctc	tctgctggaa	gcatggccag	gcctgttatt	tttcccgaat	cagaagctac	5760
agatcagaat	cagaaaacaa	aagggccaat	acttaaaatc	caaggactat	ggcatccatt	5820
tgcagttgca	gccgatggtc	aattgcctgt	tccgaatgat	atactccttg	gcgaggctag	5880
aagaagcagt	ggcagcattc	atcctcggtc	attgttactg	acgggaccaa	acatgggcgg	5940
aaatcaact	cttcttcgtg	caacatgtct	ggccgttatc	tttgcccaag	tttgtatact	6000
gttagataa	ttactctatt	ctttgcaatc	agttcttcaa	catgaataat	aaattctgtt	6060
tctgtctgc	agcttggctg	ctacgtgccg	tgtgagtctt	gcgaaatctc	cctcgtggat	6120
actatcttca	caaggcttgg	cgcatctgat	agaatcatga	caggagagag	taagttttgt	6180
ctcaaaata	ccaattcctc	gaactattta	ctcagatttt	gtctgattgg	acaaggtggt	6240
ttgctttt	tttaggtacc	tttttggtag	aatgcactga	gacagcgtca	gttcttcaga	6300
atgcaactca	ggattcacta	gtaatccttg	acgaactggg	cagaggaact	agtactttcg	6360
atggatacgc	cattgcatac	tcggtaacct	gctcttctcc	ttcaacttat	acttgttgat	6420
caacaaaac	atgcaattca	ttttgctgaa	acttattgat	ttatatcagg	tttttcgtca	6480
ctootagag	aaagttcaar	ar <i>c</i> ggatgct	CEEECOSS		CECECACCAA	6540

ggaattcgcg	tctcacccac	gtgtcacctc	gaaacacatg	gcttgcgcat	tcaaatcaag	6600
acctgattat	caaccacgtg	gttgtgatca	agacctagtg	ttcttgtacc	gtttaaccga.	6660
gggagcttgt	cctgagagct	acggacttca	agtggcactc	atggctggaa	taccaaacca	6720
agtggttgaa	acagcatcag	gtgctgctca	agccatgaag	agatcaattg	gggaaaactt	6780
caagtcaagt	gagctaagat	ctgagttctc	aagtctgcat	gaagactggc	tcaagtcatt	6840
ggtgggtatt	tctcgagtcg	cccacaacaa	tgcccccatt	ggcgaagatg	actacgacac	6900
tttgttttgc	ttatggcatg	agatcaaatc	ctcttactgt	gttcccaaat	aaatggctat	6960
gacataacac	tatctgaagc	tcgttaagtc	ttttgcttct	ctgatgttta	ttcctcttaa	7020
aaaatgctta	tatatcaaaa	aattgtttcc	tcgattataa	caagattata	tatgtatctg	7080
tcggtttagc	tatggtatat	aatatatgta	tgttcatgag	attggtcaag	agaaatactc	7140
acaaacagta	tattaagaag	gaaatatgtt	tatgcattaa	tttaagtttc	aagataaact	7200
gcaaataacc	tcgactaaag	ttgcaaagac	caaacacaaa	ttacaaaact	tataagactt	7260
aagttctgaa	ttccctaaaa	ccaaaaaaaa	aaacagaaca	tattttgttg	catctacaaa	7320
caacacaaac	ctacatagtt	tataacttac	tcatcactga	gattaacatc	agaatcattc	7380
tccatttctt	catcttcact	ctcatcatca	tcaccaccac	catgatgatt	ctcctcctct	7440
tcacgtaacc	tagcaatctc	actctgagct	ctatcaacaa	tctgcttctt	ctgcaactcc	7500
aaatctctct	gaaaatcagc	tétcatette	tccaactcct	tcatttgctc	tttcttactc	7560
ttctccatct	tctcataaac	cttcc,caaac	ctctcaacag	aatccgccaa	catcttatac	7620
gaagcagcgt	cattaacctt	cttcctctcg	tactcaacct	catcatcctc	atcctcctcc	7680
tcttcagaat	caccaggact	atccatcatc	tcatcaaacc	cattagactt	atctaaataa	7740
accttagtgt	tcataaacac	aaactcacct	gaatcaacac	cacaagctaa	acctaaatcc	7800
gacttgggcg	aaacacaaag	caacatatcc	aacttattga	aaaacgacca	tttacttgaa	7860
cctaaacctg	atttctcaac	cttaatcttc	tcttttctat	acttcctctt	caagtcatca	7920
atcattctcc	tacattgcgt	ctcagatttc	tccatcctta	gctcctcact	cactttctca	7980
gctacttcat	tccaatcctc	gttcctcaaa	ctccttctac	ccaattgcaa	aaacctatct	8040
ccccaaactt	caagcaacac	aa				8062

THIS PAGE BLANK (USPTO)

Figure 1



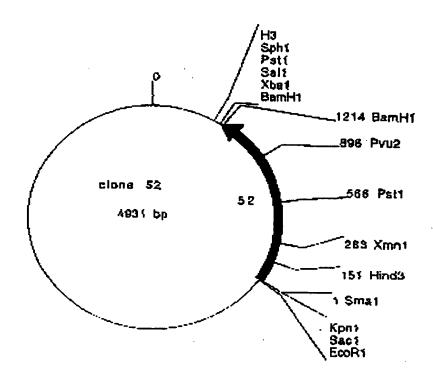


Figure 2

Comments/References: 52= 3' side of S5 (AIMSH3) 1244bp in pUG18/Sma1

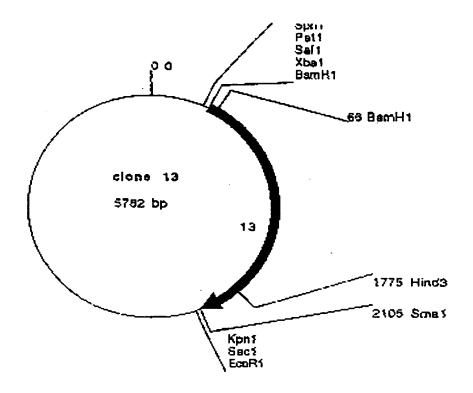


Figure 3

Commenta/References: 13 = 3' side of \$5 (AtMSH3) 2104bp in pUC18/Sms1

Ŧ
Ø
H
ē
뎚
_

30	144	204 35	\$5. \$5.	324	384	424 115	504 135	564 155	624 175	684 195	744 215	804 235	964 255	924 275
CCIAAGAAACGOGCGAAAATIGGCAACCCAAGTICGCCATAGCCACGACCACGACCTTCCATIICTCIIBAACGGAGGA	500 %	ව දුර	CIC	GAT	GTT V	A.R.G.	405 0	TIC	უ ე	ත් රථ අ	445 3	A.A.T N	GA.A.	GTT V
88	E R	e E	S S S	200	TAT	CTA	TTC	ALT N	AAT N	GGT G	CTF L	ACT S	ATT 1	GIT V
HIM	TIC	9 CCC A	53C	GTA V	GAA E	543 E	TTC	ري تري تري	G¶G ▼	S =	3 66	රූ ර	GGT	GA.
PCTC	TTC F	ACA T	TCC S	(C)	GRG B	CIG V	AGB	GAT D	CTG	TCC S) ಕ	5. S.	18 19 19	GGT
CATT	CGT H	TCA S	CIC	AHC N) () ()	ە 1 75 7	TAC	atg M	द ५ ३	SHA X	Aesa X	631	9	5
CZIC	TCT	င် ဂို	tio.a	45 O	TCG	3, 50 0	99 6.	ණ ලික	45 4 %	AIT I	204	TTT	TI.	5 5 8
೧೯೬೮	RII	ર્ફ ફુ	4 7 5	ACT T	သူ့	0 KG	TSC.	GCT A	GTG V	3	TRT	1.00 9	ACA T	FIT. I
*CC#	3 1)) () ()	CGT R	n D	វិ ភូ ដ	स्य अ अ	0	TAC Y	₽. 10: 14:	ું જું જ	TIG	ង ប	040 1340	क्षु व
92K)	Ses O	61.5 V	A A	ccr P	ರ್ ಬ	TTG L	Grr v	ATT I	الم الم	RCT P	೨೦೮	्र इ इ उ	ಸರ್ಧ S	GTT
736C	20	ည်သူ့	700 N	TCT	Tř.T F	ក្លី 🕳	ያ የ	ය බ	25 7	a A A B B B B B B B B B B B B B B B B B	rcg s	ect 6	ar Sax	ပ္လမ္
3 000	A X	#.#? E	r Cr	r L	P. S.C.A.	\$08 \$	51G	TTG L	TTC L	ACT T	CTC P	္ ဗိ	G *	GTT V
GTTC	300	0.00 0.00	n S	X EE	a Desco	TAC	а. И	ÇTG V	U で よ	50	4.05 G	វិធី ព	AG4 R	CTT V
CCAA	ON X	សូម ម	11C	100 a	S T T	R ² A	17G L	ر درور	TT	₽. K	200 8	: G	ន ខ	GGT
CARC	ပ္ ပ္	28C #	TCC S	X X	TTT E	ಸಿದ್ ಸ	GTT	වූ ය	S Z L	GTC 	ن •	SGI	GAT D	orc •
TTGG	atg	ACT T	GTA V	K P	A G	TCG S	ST S	GCB A	3	67.78 4.67.78	TTT	RET	GTG >	AGA R
ABAR		9 0 0 0	ACT.	222	శ్ర ప్రత	TC# S	GAT D	ATC	GTG V	מקד ה	רי ה	ATA I	GTT	GTT V
5350	atabacaatt	300	ည (၂)	r Z	S H	TCA S	CC P	ថ្ម ទីធ	AGT	ATT.	ទ	\$ 20 D	767 C	GAT O
AGCG	ataa	3 ×	TCC S	900	TTA	ACG.	TAC X	99.4	556	A A K	₩ ₩	97.53 23	GIT	FITT
AGP.	ACGA							OFF D						
AT 75	GATTACGA	AAA K	A. K.	000 «	202	222	AGC S	म्मू छ	A 16	955 6	RC (909	TTC :	ATG.
ret	ф П ц							505 136						

984 295	1044 315	1104 335	1164 355	1224 375	1284 395	1344	1404	1464 \$55	1524 475	1584 495	1644 515	1704 535	1764 555	1824 575
TTG L	ote v	AGC S	TTR L	GTT V	cat #	S S	AAT N	gra V	ATA I	TCC S	FTT	1550 1550 1550 1550 1550 1550 1550 1550	, GCT	R R
AGC S	TTG L	11 pa	N N	្តីដ	1 1 1 1	TTG L	A A	ACA T	TTG 1	r S	es Es	2	Crr E	A D D
TIG	FTT	361 C	GCT G	F 7	7.T'T 6	act s	GTG V	CTT L		AGT	CCT	శ్ల చ	ў.Т С М	e E
ATT	er X	GAT	ភ្ជាំ «	ဦး ပိ	ACG T	೧ ೧	GTT V	r T	₽04 8	æ ¥	a S	art I	5 TT >	rcts
ភ្នំ 🔻	9 9 3	CTG L	ನಿ ನಿ	S	82 3	T T T F	ក្ ស	ig F	GAT	e S S	61'A V	GAT U	ថ្លី ១ 4	cyc o
50€	¥ C +	arcit.	O Al H	AŢĢ	ည္မွ	S S	T:3 L	AA.T	135 0	5 00	att 1	TCT S	rta I	න්ය ි
မွှင် မွှောင်	5	in Li	स् इ.स. १	13 D	ដូន	1) 1) 1)	9	9.7G K	ج. دَأ	N TG		TC?	777¢	ال الم الم
TTA L	(1) (2) (3)	(6)	S. P.	a a a	ပ္ပ (၁) န	9 9 9	§ 0 ⊘	EAT M	CO 6	555	46. 14.	ತ್ರಾಕ್ ಸ	G 23.	ATH 1 Sont
(5) (1)	TC3 S	ង្គិត្ត ក	TGI	អូ ភូមិ	చే చేర	15 C	CJG L	ÇŞ ∓]. €5 ±	scr \$	656 13	TCI S	র ৮	့ မွာ မောင်
757 S	CIT	ត្ត។ ខ្	172 C	GCT A	GT T V	TRC Y	ACT T	říc	i) i)	S	TCT S	માઉ પ્ર) (4	CIT L
494 404	ty a	୍ଥ ଅଧିକ	ర్జ్ క	6CT	1 1	i L	£. ₹	7. 1.		ett I	GGT G	រូប ស	ች ች	CGG CTI R L Figure
r R	943 0	GPT V	rta I	GHG E	មិ្ធ	\$3C 1	ე ეე	100 \$	9 (~ %	တို့ တို့ လ	स्तुत्र ध	<u> </u>	GCT	0 G
1110 6	ر و و	() 6 6 7	GTT V	cra L	CAT H	ာ (၅) နှ	ရည် လ	ည လ)) (S	तुः स	116 2	r T	ATT
Z z	נינד	ភ្ជុំ	្រ ទី៤	r K	g S a	gy. E	crc •	atcır S	እርሉ R	GTT V	GPT V	GTC Y	000 R	7.5.8 0
GAT	TTG L	ACC T	GAT O	ATG M	rtg M	TTT E	រីក្	हु न	CII A	SCT A	TTG L	a S S	ChT x	A.A.G K
rat N	CTG	CCT	GTA V	त् स स	AAG N	ମ ଜ	A A A	න දැල	cit r	r S S	GAG B	TCC	TTT	. 8 9 9
TTC F	ញ មួយ	មួច	455 4	A X	ል 2	TTT E	સુર હ	, 150 150 150	2 K	CIT	AGT S	1	ATC I	90 9
ព្យុស្គ	A GCI	GCT	ze. Ze.	GRT D	att I	ე ი	್ಷ ಕ	gat D	30 T	000 a	S S	GTG ❖	r R R	
GAA E	4 10 10 10 10 10 10 10 10 10 10 10 10 10	E CAT	GGT	GAT	ACA		N AC	10% 8	ខ្លួ	SCT A	CTC L	cīc r	ACA T	TTP. L
TAT	3CP 8	450 A	AAT	a A	CAT H			¥ Z¥	TAI Y	TCT	C S S	TRT Y	ata I	ATT
925 276	985 296	1045 316	336 336	1165	1225 376	1285 396	1345 416	1405	1465 456	1525	1585 496	1645 516	1705 536	1765

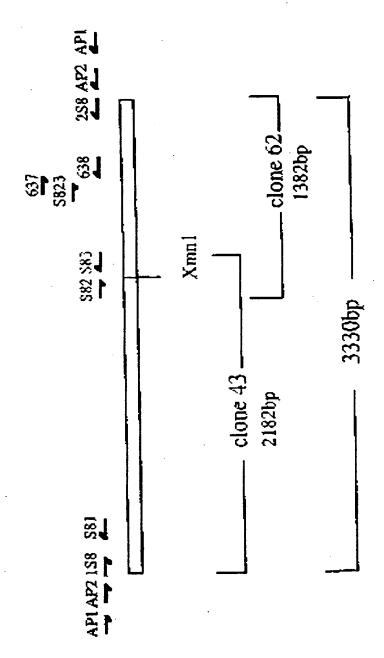
TTG ATT FCT GTT ATT TCA 1884 L I S V I S 595	CTR AAT ANG GAA GOG GCT 1944 I N K E A A 615	CAN TIT CCT GAG OFT GCT 2004 Q F P E L A 635	THE TOS ATA GET TOR ITE 2064 S S I A S F 655	TOG GGG AIC ACA CAI TIG 2124 S G I I H L 675	ara gta art rgc acc arg 2184 k v n s t k 695	UAT GRG CTA GCT CTA GCA 2244 U E L A L A 715	THE CTC ARG RGT TTC AGT 2304 F L K S F S 735	GCA CTG CAC TGT TTG CAC 2364 A L D C L H 755	GAC TIT GTG GAT GAC TGT 2424 E F V D D C 775	CIC GAG ACT AIA TIA CAA 2484 5 E T I L Q 795	CRAINTIGC CAA ATT AIC 2544 E Y C Q I I 815	CTT GCT TTR ATT TCC AIR 2604 V A L I S I 835	CTG CAC GTG CTT CAT GGT 2664 L K V L D G 855	AGA AGT ACC TYT CXA GAA 2724 R S T F L E 875
aga aaa R	7C1 GCC 8 3	ည် ဂ	CTO GAT L 0	OAN Gree	700 610 8 v 8	2	CAT AGT D S	crr cct	CGT CCC	CCT GIA	GAR 366 E 6	CCT CEB	GCC AAG	CAT GGC
CTT TTS	CIT CIC	ACT TCC	Gra Rass e X	TTT CI'T	ATC AST	CIA COT	TCG TCG S M	CAS GCT	TAT GTC Y	CGT CAT R H	CAT CCA B B B	TAT ATC	TCR TTC S F	ATC CAG
ACT C	1 44 X	atc at I T	36G G	इस्ट न ज	A HUU	277. C	CCT To	67 T	2. A. S.	SGT C	tto c e	760 T	8 8 8	AGT A
TCT s	. 66% 6	CT3	ATC I	TTG.	५	्र भू	400 K	339 1	. 7. 2. 7. 2. 7.	S TCT	e att	2 × CC	გ გ	ည ပြီး င
ಕ್ಷಾಂದ್ರ	₽ 2004 1	5 ATA	я <u>с</u> тс «	ि इ.स. इ.स.	ក ស្តី ភ	გე. ე	24K 2	6. 8. GCT) 37 N	ata crs 1 0	GAC ACA D I	GSA AAG G K	T GTB	CCT TCM
ACT GTG T V	GRC AAT 0 N	CTC GAC	GIT TTA V I.	att cga I R	GAT TCC D S	CAT CCC	att GfG 1 v	III ass f K	TCT AGA S A	AAC A1	AAT GA	රිප ජීප	TCC TIT S E	ر رور
4 H	err 6 V 0	TTG C	CCA G	GCT &	GTT G	TRI C	6CC 3	GAT I	CTA T	A 45.4 I	4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	. Pate Bate G	GGT T	ATG G
इत्य ह	א א	280	ر ان د		000	8. 8. 8.	i i	K F	ACT	ဂ် ဂ်	2£5 ^	2 ×	GTT	8.
30	get V	i i) 190	7. 14.	cje L	al'T I	CAT	Trc Y	TCA S	GTT	TTC	28 7	S S S S S S	
atc U	100 a	ج وي هر	ដូន	A.A.G K	G F F	RCT T	GAY E	* *	CTT 1	ర్ట్ 🎍	N N	ក្ ស្លា	SCT TO &	TTC
S S	700	GTT V	ទុ ទ្រឹ ធ	ည်း	a Ta	A.A.G	Ę.	A A A	1	2 2 2	GAT	A TO	ATG	CIL.
1825 576	1885 596	1945 616	2005 636	2065 656	2125 676	2185 696	2245 716	2305 736	2365 756	2425	2485 796	2545 816	2605 836	2665

2784 895	2844 915	2904 935	2964 955	3024 975	3084 995	3144	3204 1035	3264 1055	3324 1075	3397 1082	3458 5	3522 16
rra L	TTA	ata I	ACA T	GTG V	ည် မ	, AGA R	G.A.A.	62.C D	E CT3	TGA TITABICTIRACATIATAGCAACTGCAAGGICTTGAICAICTGTAGTIGCG	000 P	
ata I	ACA 4	र सु	CTG L	CTT	A CCT	<u> </u>	13 13 13 13 13 13 13 13 13 13 13 13 13 1	CAG E	AGA R	TTRE	aat R	A.A.
GTT V	ភ្ជ ២ 🗷	CCT	TAT	A.A.B.G	ATA I	CGT A	A G	E SA	ATC	rcrG	TCT	P. P
CIT	TRT	T.A.C. Y	TCG S	TRT Y	වී ය	GT.A V	ပ္ပ ပ	rct s	ag ×	#TCB	GAT	ደ ዶዶዶ
305	ည္သ	CAT H	CIC ^	cta L	50 4	S E	AGA R	្ត ប្រ	1999	Tre	ATG &	West.
CGT .	A.T.F.	50 F	is S	ĭ.ĭ.č.	CH	3CT	900	# C	SCT A	4GGT(953	The artespressranasananananana * re 4 (Contioued)
FCT	ព្រំផ	GIC	TAC Y	χς ¥	いないな	are a	5. 5. 5.	11.1 2	ዶንፕ 1	7602	iat tas asas N	terroperents (Continued)
TCT \$	ម្ចាំ ម្ចាំ	TTT F	ACS 7	GTG *	\$ CH	TTG	Gill.	2. 7. 2.	\$ % 3) ਬ੍ਰੀ ਹ	ent te	Park.
161 C	ত ব্য	CIT	99 99	5 6 F.*	£115 .÷	X Selvent	T ST	CTG L	TCG	4T2G	54.04.0 B	344 3
T CC	O#C O	GTT V	stt v	GAT D	#. . ⊀	ğa	ច្ចី ទ	ព មិ	9 9 9	CATT	୍ର ଫୁ	CCC GCA TAA AM P A A Fignre 4 (
45 44	Ç ×	TT3	r S	r F	TTT	S &	ញ្ញុំ ធ <u>ា</u>	್ವ ಕ	T COL	TRA	4 X 5	ရှင်း နှ
ATC	ACA T	TGI	GGT	GAT D	S S	સ ⊼ ડે	* *20 *4	TJ.Ľ F	AEG K	P. P. T.C.	dia ace aga aba I I R K	000 L
ATA I	AGC 5	AGH R	\$00 &	Tar Y	TTT F	r Ş	ក្ ប៉ី ធ	TTG	11.A. J.	TIL	45 45	
υ 14 12 13 14 13 14 13 14 14 14 14 14 14 14 14 14 14 14 14 14	ACT	5 2 2 2 2	7.70 ••	S SOI	3 S	at J L	র ও ও	GRC D			ACT &	S
ည္သ	ည္ဟ ဗ	សូរ ខ្	Šo	ပ္သ	2 2 2 3 3 4 4 4 5 5 6 6 6 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7	ည ဗ	atg K	GGT	ဌ မ ှင အ	11T	att a	
90g 4	કે કે કે	ಸ್ಟ ಪ್ರತ	APAC FI	A A	ည္သမွာ	ر و م	2 23	د نٔ	7'fC 8	ర్జ్ క్ల	H	ATC
E GAB	ក ភូ	CT3	AGT	GAT TAG	S S S	S æ	aca T	GCT	ర్ట్ «	r TGT	ى	≓ >-
FGT E	CIT	ပို့သ	ATC	X X	crr L	ata I	T&A ¥	S S	र्यक्ष X	_	⊢	ijο
TTA	្តិ ភូមិ ភូមិ	CAT	GAG	9 13 a	GGT 6	TGT	. 455 ×	ATT	7 100	ర్ట్ ఒ	TACTAACT	7.7G
5	GAT	9 0		776	ಸ ಭ	37.R S	SAG B	rcr s	r L L	돌	TACI	GTG V
2725 876	785 896	8 8 8 8 8	2905 936	365 956	1025 976	3085 996	3145 1036	3205	3265 1056	3325	3398 3398	34.55 6.59 6.00

Figure 5

1 WERGE	10 10 10 10 10 10 10 10 10 10 10 10 10 1	se gaessa taaspessa neabumabaraspessa sa	- D CAMPANAMER CONTRACTOR CON	OG MOGGERSTYLVERSOM BEVRYERS GLOVYBROMS VORKENDEN VERNENDER VERNER OKULOTS BESKROMENTYCKLE GFE Ge Meterakomieter acht terbeskom vor beskromen vor beskromen vor beskromen van ver beskromen van ver beskromen	THE STATES OF ST	ye otusetyerournentrourus versus sylvetes sylvetes sylvetes sylvetes sylvetes sylvetes sylvetes sylvetes solvetes solvetes solvetes sylvetes sylves	90 BEGVESSTVORFIGATERVERVERVERVERVERVERVERVERVERVERVERVERVE	6 4	STATE OF STA	TO SETELEMENT OF		
¥ 5		50 19	70 21 30 21	0 0 7 0 8 0 8 0 8 0	 	• • • •	10 C	<i>ور ون</i> ون بر 44 44	* C	- U & M	9 6 4 8	- Mt 10
1 				* X X X X X X X X X X X X X X X X X X X	X SB D.	# E E		**************************************	# # # # # # # # # # # # # # # # # # #		89	होता संश स्टब्स स्टब्स

Figure 6



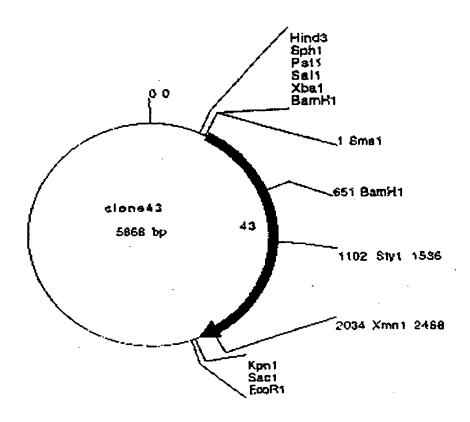


Figure 7

Communits/References: 43. 5' side of S8 (AIMSH6) 2182 by in pUC18/Sm81

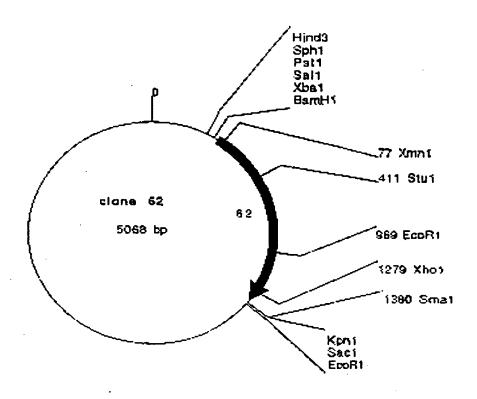


Figure 8

Comments/References: 62= 3' side of S8 (A1MSH6) 1379bp in pUC18/Smat

သသ	G	TCC S	989	AGP R	000 4	₹ ×	GAT	XAA K	S S H	GCT *	GTB V	क् सु	₽. R R	77C
agtigagocotiga ogaga atogitto og catticta ogago daroga ogaga attittogogo da tottogogo	9 0 0 0	GIT	S PS	GTT	æ& ≉	GTA V	rat 8	GCT 6	GTA	R.	CCT	ž Ž	75. 7	GTT
atct	ပ္သ ဗ	17G	ALAG R	වසුය ව	TTT E	TTT F	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	P. T. T.	rca S	8 .	GTT	P.P.G K	8	GBT D
5 5 5	2 0 0	GST	516 V	GAT	§ 6	A A	ပ္သည	z Z	AGA R	R 251	N N	3	GAT	CCT 8
166C	a atg M	AAC A	AAT N	GTC	rcr	त्रुप्त स	GTT V	700 8	crr t	atg 8	GAT D	4 કું ગ	# GG	ರ ಕ
TTTT	AAAA	7	TTT F	TCT \$	្ត្រ ទ	я Б	513	C(5.1	មិ មិ	9 9 9	CHO T	761 C	TA I	ATA
ARAĤ	TTCC	ECT T	768 3	4 4 4	ر د. ريو	ATT	CAT	- L	بان در ان	ට් 10 ක	A.S.	GT'S V	មិ មិ	ည့် ဘို့ အ
9000	#CP.	5 5 5 6	න් වූ	TCG S	۲ وا ت	aat B	्र इ.स.च्या	440 C	AG\$ X	ACA T	TT J E	ဗ္ဗာ	TCT S	TTE L
GCAA	TCTC) 209 20	ტ ტ	GIT	CGT R	150 R	§ ≈	್ ₽	9 0 0	4 4 5 8	F.	G&1,	s s	کړ ۲
CGAC	TCIC	1.	§ 0	100 a	CGT R	मूम् ह	AGC S	ATT I	res S	(CC)	atg M	5 A A	១ ខ្លួ	7. 7.
TCTÀ	TCAC)))	3.55 S	T T T	000 A	្តិ ប្	34GG R	5.C.\$	7 7 7	SG t	a A	;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	CIT	A A A
CATT	TCIC	a a	၁၉၁	R	GTT	77. \$	SAG E	GAT D	e; s	ري 1	Ç U	atg N	TGG N	CAT
0000	TTTC	্যুম ১	ည ဗ	GT.9 V	AAG K	700 5	₹ <u>0</u> 0	। भूष	TTT E	GTT V	3 3 5 3	4. 4. 7.	ក្នុង ស	TRC
GTTE	ATCG	TIC	1939 194	TCT	0 19 19	हुत् इ.स.	TCT	SCT B	ect A	GAT D	CTC L	5 5 7 7	TTT E	CTT
XAIC	arra C	TTC	ည ဗ	GCT A	၅၂ ၂၂ ရ	GAT D	TGT C	A X	CAT H	ស្ងួ	GTT V	7 30 x	축	8 4
SCAG	CICA	rcr	25 s	ပ္မရ	5 .	GST G	GAT	A TG	7.8 0	GAT D	కే క	# # X	ACC T	GAT O
TGA	70.60	2	13 et	i i i	i E) ಶ	8 8 8	to to	AGA R	GTA V	A A	AAC	ថ្ង ២ ២	CAT
) OS Se	graticicaceccarrentestics of the contraction of the	ATT	SCT &	A X	CAT.	10C	GAT.	CTA L	क्ष क	g g	TTG	S	S. S. S.	7 7 7
TIC	BART	TCG 2	GAT (GCT &	#CG	ត្ត ទី	c E	act S	180 a	ATA I	بر ال	ည်း ရ	A.F.C	cgr R
3	. X	- 07	-				_			_	_	48		-44

993 28¢	1053 304	1113	1173 344	1233 364	1293 384	1353	1413	1473	1533 464	1593	1,653 504	1713 524	1773 544	1633
ATT	105 t	100 t	GTT V	r ath x	999 0	r TCA S	S ATC	s gra	r Acg T	s GAT D	A TCA	A GAG E	r ttt P	7 GAG
Ha	TTR L	GIT 8	독자	rci 1	ATC 1		St St	AAG K	Trt Y	ACA T	ក្ មិធ	.	ATT 1	CITY.
74 C C	S S S	0 0 0	TAT Y	AAT	AAC X	F.A.G	មួ ២	T CCA 2	A A	GAT	S	CTT	ភ្ជុំម	Z Z
IAT A	လ လ	eg k	క్రే ల	GCT	න් ලි ප	a So	GTT V	7CT 5	₽66 ¥	9 9	1 <u>7</u>	ಕ್ಟ	88 8	GTA V
म् म्	GAT	150 C	ದ ಭ	scr G	GAG A	r U	₽ \$	GTT	CTA J	A TG	ក្រុក ភូមិ	S S	Cr.	ATG N
رگ در	CTA	र् <u>द</u> द	E E E E	AGA R	8 60	040 E	TTT	0 0	ii ii	GTA V	an K	CT7 L	A.S.G	9 L =
raga X	្ត ស្ត្	13 13 19 19	TTA	U U U U	۾ 15 ه	ភ្ជ ភូមិ	P P	r N	2,3,6 K	4 5 6	T:[3	ပ ပြုတ်	CTT.	NI GGC CNG AC G Q T (Continued)
STT &	# >-	576 v	स् राज्य	જુ સં×	ર્યું . •	i i	17G	11G L	ž,	7 P		STT V	GT.	GGC G Sonti
ksr c	7. 1.	SGT C	25. 25.25.	605 A	લ () લ	ATC I		ITA L	ಕ್ಷ ಕ	GTA V	ကို ဗြိမ	Cat o	GAT	ந்சு
D %	ည် မ	n S	ಕ್ಷ ಕ್ಷಿ	ឡ ប៉ុ	r S S	ក្ ស្ត្	GCT	ტეტ ∢	egy L	ဂ ္ဂ	2 2 2 3 3	7. 10.1	GA.S.	ATT I
TAT 1	TRI Y	ATG M	GTG y	GAC D	ACT T	ą ą	TGT	: : :	ಸ್ಪರ್ ಸ	Ş"	TCT S	ခို့ ပိမ	CTA	AGA P
0.00 1.00	rit F	ರ ಕ	600 4	13.03 S	TTA	5 T		دنتا	ري دي م	57G 2.	ភ្ន ស្ត	aat N	og ×	ב ט
eAG K	AAA K	at B	3 3	4 1) 4	GTÀ √	£29 ¥		607 8	ťı	g a	ata I	ក ម្	CTA	វិទីវ
₹∝	000 9	245 K	GAT	Q.₹.	ე 0. შ	CTT L	TTT F	() 4	្ត ទ	GTA V	4.10	6.61 6	7. 10.05	
ဦးက	GTC V	₹53 3	а та 1	CTA	GTT V	crr	GCT *	TCT	44.7	00 8	aat M	Q T	TCT	AG6
ົ ຊິ່ງ ∢	ቶይች X	GAC D	, 15, 0	9 5 0	CT3	r F	TTT E	ACA S	age S	acg T	AGA R	G 1 T	CTG	747 Y
ည်းအ	TIT E	ព្រះ	a EGT	9 9 9	AAG K	GTC	ğ o	5 8 4	ည် ဝ	TTT S	GTT V	GCT P	ខ្លួ	ÇTT V
11G 1	TIC	ក្នុង ខ្	₹ 3 ⊔	A.T.C.	A R	ပ္တန္	TRT Y	GAT T	TH.	999 9	603 5	TGF	AAT H	ର୍ଷ ପ ଅପ
ž X	CTT L	#.#G *	s	S R S	<u>ရ</u> ပိပ္	GAT D	GTG *	GAT.	TTA L	₹ 1	135 4	8.45 18	ATT	T TAC
aac aaa atg K K m	GTG V	CAC H	XTC I	ଜ୍ୟ ଜ	at I	5 15	ACT	AGC S	GTG V	TTG L	5 ₹	7 00 50	्राप्त	K
934 265	996 285	1054	1114 325	345	1234 365	1294 385	1354	1414	1474 445	1534	1594 485	3654 505	1714 525	1774 545

\$DOCID: <WO 001040282TI >

1893 584	1953 604	2013 624	2073	2133	2193 684	2253 704	2313 724	2373 744	2433	2493 784	2553 804	2613 824	2673 844	2733 864
												•		
A A	GAT O	agt S	ပ္ပ	GTG V	CAT E	A.A.A. R	ರಿ ರ	ACT	C.S.C H	600 6	5 L	GGT	att I	R R
GAT	ል የ	CAJ. E	4 5 5 5	ess K	l I	161 C	g «	सु सु	att 1	GCT	ξ. X	20	AGC S	r C
E TO	CIC L	ភ្នំ ភ	CIC	ξξ. Α	4 555	CTC	क्षु ध	GCT *	67¢	TCI	0 0 0	33 4	ဂ ဂ	2 7
TAT Y	e E E	Mac N	CIG L	0 0 0	rgt S	Z ×	777 F	7. ₹	ម្ភា ម	ည်သ	PAT' N	g 4	AGT	ACT T
ž Ž	E E	GC.3	ag a	ر. ال ال	र १५ १५	TAT Y	දී ය	ရှိ ဖြ	rcr s	P G.	n Sec	GTT V	AGC S	5 4
TAC	i i i	ACG I	4 5 9	C:1	:• :•	ון מון בין בין בין בין בין בין בין בין בין בי	T T	9. 1.	76G	₹ 80	SAT D	5 4	AGA R	X X
TTG L	a.ic I	7.T.C.	47.	(; (; e;	<u>ب</u> ن ن	175 1.	C:T	ACR.	ಕ ೧ ೨	500 es	7 7	Til	ACA R	SGF S Trivied
A CC	7GG	स्ट्र इ.स.	کېد ≃ کا	٠. ن ء.	\$ %	۲:۰ چ	T : T		a T	7 12	sct å	g a	SCT *	13 to 2
999	raa 1	લું કું ઉ	n S	13 14 14 14 14	CTC ¥	: ಚ	f1				6. 19. 14	CAT R	GAG X	ATG M 9 (C
S S	76G	GTT V	CTT	516	AT:	0 1: 4: 21	១ ១ ១		છું _જ	म्म म	ភ្ជី ស	a S	ပ္ပဲ	CCA ARC P N Figure
ניין יי	TTA	er S	X X	ici S	නු වී ලා	# # ±	CJR 1	ಲ್ಲ ಇ	તું. છે સ	₹ S	Я́ З	CTS L	ಣ	
S C	CTC	G&T D	S CAC	00 K	Ç U	្តិ	្តិ ស្ត្រ ស្ត្រ	တွင် တွင်) 2 (1)	494 6	8 ~	ង ប្រ ១); 	60 60 60
GGT	A B B B B B B B B B B B B B B B B B B B	CJ.	01.0 1	န သ န	TTT F	e G	S S S	7. Y	TTÏ	CTG L	777 F		ATB I	ACG T
GAT	X X	13 C) #4	TRT X	Ę N	္က် (၂) ရ	X Sign	at a	بة يو ح	r L	GTC V	ATT	ATC	GAT	or T
ig U	GGT	X X	2 2 2 2	₹ ~	45 X	 3 0	GGA G	۳. دن	3 3	GAT D	GTT V	ž Ž	ZŽT ¥	TTA L
ည္ကမွ	ACT T	AAT	ပ္သမ္	GT T V	SIT V	CT.	STP >	Titi F	PTC I		CCI	CII	ပ္သည	TTĞ L
PAT	5	ATC	मुद्रा	8 S	چ وي ه	SCT A	ITA L	ပ္ (၃ ၀	CTT L	ត្តិ	256 R	ATA	GIT V	S S
AAC H	AGT S		ATC	ICT 5	300	77G L	ATA.	ر م م	ata I	ည်း ၁၁	ည လ	\$ \$ \$ \$	ದ್ದ ಕ	9 9 4
TTT	GTT	EMB 5	కే చ	HAG X	አ አ	TTG L	CCT	GAT	a S	ATA J	atg K	ମୁମ୍ବର ଜ	7. 2.	CCT P
ATA	151	618 V			CJG	CTG			r L	ACC T	AGC S	A A A	45 o	CAT
3834 565	1894 585	1954 605	2014 6 25	2074 645	2134 665	2194 685			2374	2434	2494 785	\$652 \$608	2614 825	2674 845

2793 884	2853 904	2913 924	2973 944	3033 964	30.93 30.93	3153	3213 1024	3273 1044	3333 1064	3393 1084	3453 1104	3521 5	3579 1.9	3606 28
rv 40	CA Q3	CA QA	14 41						_			_		
7.6C	4 t	act T	TAC Y		A A A		GTG v	ου «¢	s s) (1)	i i	CTC	P.P.A K	
101 S	ATG	4 4 4	g o			ಕ್ಷ 2	కే రీం	3 &	TCR S	HAT H	3 S	160C1	É.	
CAG E	ATC	z z	GRT D	atg M			Cit	GCT P	71C	A. A. C.	A A	TTT	cga tta r l	
16 1	AGA R	9 3 o	TTC	000 8			క్రో ఆ	GCT A	ପ୍ରକୃତ . ଜ	2 E	3 ATC I	ACA TAA CACTATCIGAAGCICGITAAGICTTIIGCCICTCI T	រូប្រា	
ರ ೯	GAT	13	ACT T	1GT C	R 61	ភ ភូមិ	TAC	G GT	1 TCT 5	900€	040 a	cort?	TTT (
GTG V	rcT \$	GiT V	AGT S	ಕ. ಬಿ.	80	CGT *	25 R	7 T.S	40% R	4 GTC	E H	AGCT	130	. স্থি
78C *	ನ೧ನಿ ೩	င်း လ ပုံ	AC.t	str ,	Ç K Ç	S. D.	ည်း သည် သ	स्ट्र ी स	3. CTA	ಕ್ಷ ಬ	r TGG W	CTGP	3 ×	figure 9 (Continued)
7 0 0	ם ט	95 A	600 6		พานีโ	A A	CCT	T T	្ត ទី ធ	r TCT S	TTR	CTRE	A X	[Con1
ည္သ ဗ	CIT	a E	AGP. R	ឡ ដែ	00 ≪	Tr. Y	161	ଖୁଣ୍ଡ ଅ ଜ	1 AG"	r git I	7 7GC C	3 3	ATC	خ م
7	i S	្ត ទ	ည ဗ	GTA V	TTC ₹	GAT D	SCT.	GT'F	S TCA	. CG3	: TTT F	₹.	TAT	lguse
ో ప్రా	३ ८३ १	acT T	ຄຸວ	CTG L	in SA	रदर §	ភូពិ ភូ	() () ()	\$ %	ស្រ		i at ⊨	TTA	_
) 3 4	TTC	76C	ਬ੍ਰਹ: 2	CAC TO	X X	\$ 50 50 50 50 50 50 50 50 50 50 50 50 50 5	S S	44.5 Q	71.FC	1 17G	T ACS	r ATG N	160 0	स स स स
TTT E	arc I	के स	GAC D	೧ ೧ ೯೪	a Turk	Ų.	A AC	#. 14.3€	AAC R	e E E) 685 0	©CT ₹	A X	ब इ. रू
ATC	<i>ል</i> ር፣ 1	GTA V	CET	TT.	CIC	ል ማ	TTA L	ე შ	ស្ល ១ ១	54.4 K	T P	, atg	# Y	स्तुस स प्र
, 5. 7. 7	\$ 0	T O	aTC I	GTT \$	1	TTC	CGT R	ata I	5 5 6		282 0	TAR.	CTT 3	# **
႘ၟ	0 7 7	T T	GTA.	375 8	Ç\$0 ₩	4 4 4	1åC ⊀				SAT D	ž×	8 CT 9	A A A
CTG) 1	T CC	i i	TAC ₹	T AC	4 60	TTG	SCT A	្ត្រី	3.4C		€ € € €	HT.	A. 75
rer			ដ្ឋ	ញ ប្រធ	ರಸಿಗೆ ಚ	CCT Section	TTC						£	A ARA
DA L					ACA T	atg X	org >	C C T	RATE I				RTG II	4 A
60 A		្រ សូម ស្រួម				C. F.C.	CTA	90 A	ATG	: ភូមិ) D	, TAC	(C)	RAA
23 40 70 70			2914 925	2 5 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	3034 965	3094 985	33.54			3334	3394	3454	3522	3580 20

Figure 10

A A A A A A A A A A A A A A A A A A A	50
PPTTTTGGTTGCTAACAATAAAGGTATACGGTTTTATGTCATCAATATAA	100
TATATATAAAAAAAAGAAATATATATTATTTTTTCATTTATCAAAC	150
APARCARCAAGACTTTTTTTTTACTTTTTACATTGGTCRACAAAATACAA	200
CATAAACGACATCGTTTAATCATTTCCCAATTTTACCCCTAAGTTTAACA	250
CUTAGAACUTTCTCCATCTTCGERAGCACAGCCTGATTAGGARCAGCTTT	300
ACCATTCTCATATTCCTGAACTACCTGAGTCCTCTCATTGATCTGTTTCG	350
CCAAATCCGCTTGTGACATCTTCTTCTCCAATCTCGCTTTCTGTATCATC	400
AACCTCACCTCTGCTTTCACACGATCCATCGCCGCAGGCTCTGTTTCTTC	450
TTECAGETTETTETCTTAATCACCGGAACCGCCGTAGATTTCCCCTTTT	500
TGTTCGAACCGGCATCGAATTTCTTAACCGTTTGAACCGCGACACCGTTT	550
CTCAGAGCTGCGTTAACCGCTTTCGGATCGCGTAGGTCTTGGCTCTTTTG	600
TTTTGATTTGTGGAGAACTACTGGTTCCCAGTCTTGTGTTACTGCTCCTG	650
GGTATCTGCTCGBCATCGTCGATGAATTGAGAGAAAGGAACAACGCCAAA	700
ATTTTATTAATCTCAGTTTTGAAATTGAGAAACGATGAAGATGAAGAATG	750
PTGTTGAGAGGATTETGATATTATATACGAAGATTGGTT7CTGGAGA	90 0
ATTCCATCATCTTTTCTCCATTTTCCTCTCTGGAACGTTCTTAGAGATG	85 0
NTTGRCGACGTGTCATTATCTGATTTGCAGTTAACCAATGCTTTTTGGGT	900
TREATTCRTGGTACACCATATTATCCGATTTGGCTCANTGGTTTTATATA	95D
ARTTTGGTTTTCGGTTCGGTTATGAATTATGATTAAAATTAAGGTAACGA	1000
BEARTTTTCGTRADATTTATTTCGGTTTCAATTCGGATCCCTTACTTCCA	1050
CARCOGRATIATTCGARACCOGGGTTARCCGRACCGRATACCRATGCCTG	1100
PATER LACGET GECTAGARAGA (CCARCUCTATACARTAGARCATAA	1150
NTCGCACGGTCATCAAAGCCTCARAGAGTGAACAGTCAACAAAAAAAGTT	1200
GAGCCCTUAGGAGTATCGTTTCCCCCCATTTCTACGACGCCAAGGCGAAAAT	1250
TTTTGGCGCCAATCTTTCCCCCCTTTCGAATTCTCTCAGCTCAAAACATC	3300
CTTTCTCTCACTCTCTCTCACAATTCCAAAAAATGCAGCGCGAGAGAT	1350
CCATTTTCTCTTCTTCCAAAAACCCACGCGGCGACTACGAAGGGTTTG	1400
CTTTCCGCGATCCTGCTAGCGCGCGCGCAGCGGAGACCACCACTTT	1450
AATCTGAAGGAAGGGATGCTAAAGGCGACGCTTCTGTACGTTTTCCTGT	1500
TTCCARATCTGTCGATGAGGTTAGAGGAACGGATACTCCACCGGAGAAGG	1550
TREESCATERIATES CONTROL TO THE TRANSPORT OF THE TRANSPORT	1,600
CATGCTTCGTCCCTGTTCTCCAATATTATGCATAAGTTTGTAAAAGTCGA	1650
TGATCGAGATTGTTCTGGAGAGAGGTACTARTCTTCGATTCTCTTAATTT	1700
TCTTATCTTTAGCTGGAAGAAGAAGATTCGTGTAATTTGTTGTATTCGTT	1750
GGAGAGATTCTGATTACTGCATTGGATCGTTGTTTACAAATTTTCAGGAU	2600
CCCLGAAGATGTTCCCCCTGAATGATTCATCTATGTATGAAGGCTA	1850
> 1/2 TETTRITCETCANTITOSTTCERATARTGETAAARCTCAAGARAGA	1930
AACCATGCTTTTAGTTTCAGTGGGAGAGCTGAACTTAGATCAGTAGAAGA	- -
TATAGGAGTAGATGGCGATGTTCETGGTCCAGAAACACCAGGGATGCGTC	1950
CACGTGCTTCTCGCTTGAAGCGAGTTCTGGAGGATGAAATGACTTTTAAG	2000
GREEATRAGGTTCCTGTATTGEACTCTAACAAAAGGCTGRAAATGCTCCA	2050
GGATCCGGTTTGTGGAGAAGAAGAAGTAACGAAGGAACCAAATTTG	2100
AATGGCTTGAGTCTTCTCBAATCAGGGATSCCAATAGAAGACGTCCTGAT	2150
CATCCCCTTTACGATAGAAAGACCTTACACATACCACCTEATGTTTTCAA	2200
DATE OF THE PARTY	

		2250
GAAAATGTCTG	CATCACAAAAGCAATATTGGAGTGTTAAGAGTGAATATA	2300
	CTTTTCTTAAAGTGGTTAGTAACTATTAATCTAGTGTT	2350
	CTCAATGTGATTTGTTCACTTACATCTGTTTACGTTATG	2400
	GGAAATTTTATGAGCTGTATGAGCTAGATGCGGAATTAG	2450
GTCACAAGGAG	CTTGACTCGAAGATGACCATGAGTCGTGTGGGAAAATGC	2500
	TTACTTGAAACAACTGGCCTGCTTGAATTATTGTGTCTA	2550
	ACCACCTTTTGTTTCAGGTTCGTATCTCTGAAAGTGGGA	
	gtgcaaaagctattagctcgtgggtaagggaaccatcat	2600
	nticotitactoctacttcoctassatitaasaaatgga	2650
	gcatcattagttaggatcetgagaacteaggatgttte	2700
	rtaataagtettterteraggagtarerarcaaactt	2750
BCACAATATT	TODAKTOBASSATKIKATASBOKASBOTSASTTOTOTOTOTO	2800
	tstagtaacagttacggataatatatgtttacttgtatg	2950
TGGTACCCTC!	attttgtctctcatggaggctttgaageettgtgttgaaa	2900
CTGGATAGTT	RCATATGCTTCCAACAGAAACTAGCRTGCRGATTCATATG	2950
CTTTCCTATI	/ADTTTTTTTTOTCOCACACACTCATATOTTTATOATO	3000
agatataaag	Kaaddaadtaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	3050
AGCCAGAGGT	DTDADAGDAGDAGTTTTTTTTTGGATAGGTCAAGGAGAGTG	3100
TTGCAGACTG	TETTTEATCATTTCTTTTTCTGTACATTACTTTCATGCTG	3150
TARTTARCTO	AATOOTTATTOTGSTCTGAYTATCAGATAATTOTAACAAAAAAAAAAAAAAAAAAAAAAA	3200
GCTAGTTCAG	DDDDTTAACKKADDGAGCAACOACCTACTACTTGCGC	3250
CTGATGCCGT	CCATUTTCTTGCTATAAAAGAGGTTTGTTATTTACTTATT	3300
TATCTTATEA	TOTTCRGTTCATCCAAGTCCTGAAAAATTACACTCTTCTT	3350
TACCAATCTT	CCATCAAGCTGTGTAAAGGATTTGGGAAAATCATT	3400
atttgatcc7	TTGTTTTATATCCAAGAGATCTCCTTCAAAAGATCTCTTTT	3450
AAGATTETTT	GCACTTGRAAAATTUAATCTTTTTRAGTCAATCCCCTACT	3500
ТРАЗИТСЭТТ	GATCATAGTCTGCATTGCATGTCAAGTAATATCATTCCT	3550
75TTACT9CA	atscccetetticttratgacentigtctatgttgtsttig	3600
TCTCGTGTGC	togagaaaatgatagctgateeaagctctacatta1'catg	3650
	TGCTCAGGAATTGCCTTTGGTTACATTGCCTAATGGY17G	3700
	TTCTTCTGAATCTTTATTTTAGATCAAAATGGAGCTACAA	3750
ANGTGTTCN	actetgtatggatttgctttgttgactgtcctgccttgag	3800
GTTTTGGG7	iggctccatcagcgatgaigcatcaigtccigctcttggag	3850
	tgcaggtaagcaagtgtattetgtatctatgtatgtaccatg	3900
TGACTTCCT	GTGCATATATTTGGGTTGCAGGAACTAATTCTGAATCACCA	3950
TTTGTAT6	TTTTTTCCAGGTTTCTCCAAAGGAAGTGTTATATGACAGTA	1000
ARGCYARAC	TECTTGTATCGCCAGTTGTTTTGTTAAACAGAATTTAAGGT	1020
ABATGAGAG	TGGTTAATTTAAAGTGCA1ACATGTTGAAA1ATTGCAGGGC	4100
PATCAACIO	AAGCACAAAAGGCTETRAGGAAATATACGTTGACAGGTACC	4150
17. COMONA 17. COMONA	GGCAAGCTAACTGACAATTTAACCGCTCACCGAATGATAGG	4200
7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CATTGCTAATGTAGATCATGTTTATGTTTCAATCTAATAGG	9250
CALCATACO	GGTACAGTTGGCTCCAGTACCACAAGTAATGGEGGATACAG	1300
74/2545C4C	GAGTTAGAAATATAATAGAATCTAACGGATACTTTAAAGGT	4350
かんかいしょう (7	TCATGGARCTGTGCTGTTGATGGTCTAAATGAATGTGATGT	1400
101101000		

TGCCCTTAGTGCTCTTGGAGAGCTAATTAATCATCTGTCTAGGCTAAAGG	4450
TOTOTTGSCTIGTTTAGTTTTTGCTTTTCACAAATTAAGCAAAGGAACTT	4500
TTCATAACTTACAGTTTCTATCTACTTGCAGCTAGAAGATGTACTTAAGC	4550
ATGGGGATATTTTTCCATACCAAGTTTACACGGGTTGTCTCAGAATTGAT	4600
CCCCASACGATGGTAAATCTTGAGATATTTAACAATAGCTGTGATGGTGG	4650
TCCTTCAGGCARGTGCATATTTCTTTTTTGATAACTTCAACTRGAGGGCR	4700
GACATAGAAGGAAAAATTCTAATACTTCGTACGGATCTCCAGTAAGTA	4750
AGCCGATTTTGTTTACCTATGTAGGGACCTTGTACAAATATCTTGATAA	4900
CTGTGTTAGTCCAACTGGTAAGCACTCTTAAGGAATTGGATCTGCCATC	4850
CACTCARAGATGTAGAAAGCATCAATAAACGGCTTGATGTAGTTGAAGAA	4900
TTCACGGCAPACTCAGRAAGTNTGCAPATCACTGGCCAGTATCTCCACAA	4950
ACTTCCAGACTTAGAAAGACTBCTCGGACGCATCAAGTCTAGCCTTCGAT	5000
CATCAGCCTCTGTTGCCTGTTCTGGGGAAAAAGTGCTGAAACAA	5050
COAGTAAGTATCACACAGTTTTCTGAGTAATGCCTTCCATGAGTAGT	5100
ATRGGACTARACATTRCGGGTCTACCTARGRCTCTTCTCCCTTCTTTTG	5150
ATAGGACTARARCATTACOGGICIACCIDAGGI	5200
CAATGTCTGGTTATTCATTACATTTCTCTTAACTTATTGCATTGCAGGTT	5250
AAAGCATTTGGGCCAAATTGTGAAAGGGTTCAGAAGTGGAATTGATGAGTGTT	5300
GTTGGCTCTACACAAGGAATCAAATATGATGAGTTTGCTT7ATAAACTCT	\$350
GTAAACTTCTTATTAGTAGGAAAAAGCCGGCTCATTTTTTTT	5400
CAATTCGAAGCAGCCATAGATAGCGACTTTCCAAATTATCAGGTCCCCAT	5450
CTATCTTTCATACTTTACARCAAAATGTCTGTCACTACTCAAAGCAATGC	5500
ATATGGCTTAGATCTCAACTCACACCCCGAGGATCCTAAAGGGATTTGCT	5550
TTTTATTCCTAATGTTTTTGGATGGTTTGATTTATTTCTAACTTGAACTT	5600
ATTAATETTGTACEAGAACCAAGATGTGACAGATGAAAACGCTGAAACTC	5650.
TCACAATACTTATCGAACTTTTTATCGAAAGAGCAACTCAATGGTCTGAA	5700
GTCATTEREACCATARGCTGCCTAGATGTCCTGAGATCTTTTTCCCGAAT	5750-
AGCARGTCTCTCTGCTGGAAGCATGGCCAGGCCTGTTATTTTTCCCGAAT	5800
CAGAAGCINCAGAYCAGAATCAGAAACAAAAGGGCCCAATACTINAAATC	5850
CAAGGACTATGGCATCCATTTGCAGTTBCAGCCGATGGTCAATTGCCTGT	5900
1CCGRATGATATACTCCTT6GCGAGGCTAGAAGAAGCAGTGGCAGCATTC	5950
ATECTCGGTCATTGTTACTGACGGGACCAAACATGGGCGGAAAATCAACT	6000
CTTCTTCGTGCAACATGTCTGGCCGTTATCTTTGCCCAAGTTTGTATACT	6050
dgttagataattactetattetttgcaatcagttcttcaacatgaataat	. 6100
AAATTCTGTTTTCTGTCTGCAGCTTGGGTGCTACGTGCCCTGTGAGTCTT	6150
GCGAAATCTCCCTCGTGGATACTATCTTCACAAGGCTTGGCGCATCTGAT	6200
AGAATCATGACAGGAGAGAGTAAGTTTTGTTCTEAAAATACCAATTCCTC	6250
GAACTATT7ACTCAGAT177GTCTGATTGGACAAGGTGGTTTTGCT77TT	-6300
TTTAGGTACCTTTTTGGTAGAATGCACTGAGACAGCGTCAGTTCTTCAGA	6350
ATGCAACTCAGGATTCACTAGTAATCCTTGACGAACTGGGCAGGAACT	6400
agtactttcgatggatacgecattgcatactcggtarcctgctcttctcc	6450
TTCAACTTAYACTTGTTGATCAACAAAAACATGCAATTCATTTTGCTGAA	650ú
ACTTRITGATTTRIATCRESTTTTTCGTCRCCTGGTAGRGRARGTTCART	6550
CTCGGATGCTCTTTGCA4CACAT7ACCACECTCTCACCAAGGAATTCGCG	6601
TCTCACCCACGTGTCACCTCGAAACACATGGCTTGCGCATTCAAATCAAG	6001

atctgattatcaaccacgtggytgtgatcaagacctagtgttcttgtacc	6650
GTTTAACCGAGGGAGCTTGTCCTGAGAGCTACGGACTTCAAGTGGCACTC	6700
atggctggaataccaaaccaagtggttgaaacagcatcaggtgctgctca	6750
AGCCATGARGAGATCAATTGGGGAAAACTTCAAGTCAAGT	6800
CTGAGTTCTCAAGTCTGCATGAAGACTGGCTCAAGTCATTGGTGGGTATT	6850
TCTCGAGTCGCCCACAACAATGECCCCATTGGCGAAGATGACTACGACAC	6900
*TTGTTTTGCTTATGGCATGAGATCAAATCCTCTTACTGTGTTCCCAAAT	6 9 50
AAATGGCTATGACATAACACTATCTGAAGCTCGTTAAGTCTTTTGCTTCT	7000
CTGATGTTTATTCCTCTTAAAAAATGCTTATATATCAAAAATTGTTTCC	7050
TCGATTATAACAAGATTATATATGTATCTGTCGGTT7AGCTATGGTATAT	7100
AATATATGTATGTTCATGAGATTGGTCAAGAGAAATACTCACAAACAGTA	715D
TATTAAGAAGGAAATATGTTTATGCATTAATTTAAGTTTCAAGATAAACT	7200
GCAAATRACCTCGRCTAAAGTTGCAAAGACCRAACACARATTACAAAACT	7250
Tatargacttargttctgaattccttaraaccaaaaaaaaaa	7300
TATTTTGTTGCATCTACAARCAACACAAACCTACATAGTTTATAACTTAC	7350
TCATCACTGAGAT TAACATCAGAATCAT TCTCCATTTCTTCATCTTCACT	7400
CTCATCATCACCACCACCATGATGATTCTCCTCCTCTCACGTAACC	7450
TAGGAATCTCACTCTGAGGTGTATCAACAATCTGGTTCTTCTGGAAGTCC	7500
AAATCTCTCTGAAAATCAGCTCTCATCTTCTCCAACTCCTTCATTTGCTC	7550
TTTCTTACTCTTCTCCATCTTCTCATAAACCTTCCCAAACCTCTCAACAG	7600
AATCCGCCAACATCTTATACGAAGCAGCGTCATTAACCTTCTTCCTCTCG	7650
TACTCAACCTCATCATCCTCATCCTCCTCTTCAGAATCACCAGGACT	7700
ATCCATCATCTCATCAAACCCRTTAGACTTATCTAAATAAACCTTAGTGT	7750
TCATAAACACAAACTCACCTGAATCAACACCACAAGCTRAACCTAAATCC	7800
GACTTGGGGGAAACACAAAGCAACATATCCAACTTATTGAAAAACGACCA	7850
TTTACTTGAACCTAAACCTGATTTCTCAACCTTAATCTTCTCTTTTCTAT	7900
ACTTCCTCTTCAAGTCATCATCATCTCCTACATTGCGTCTCAGATTTC	7950
TECATCETTAGCTECTCACTCACTTTETEAGCTACTTCATTCCAATCCTC	900B
GTTCCTCARACTCCTTCTACCCAATTGCRAAAACCTATCTCCCCAAACTT	8050
CAAGCAACACAA	8062

Figure 11 (Continued)

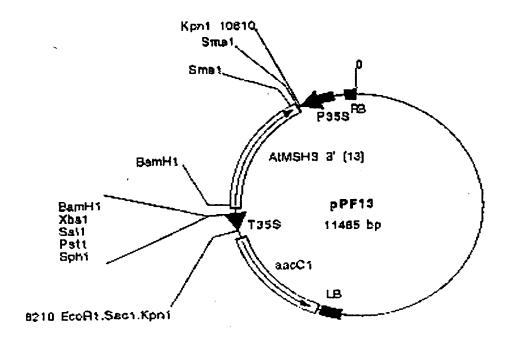


Figure 12

Commente/References: AtMSH3 3' side antisense : AtMSH3 3' (19 = 2104bp) from pUC18/13 Sal1/Sal1/T4 into pCW184 BamH1/T4 In Agrobacterium LBA44O4

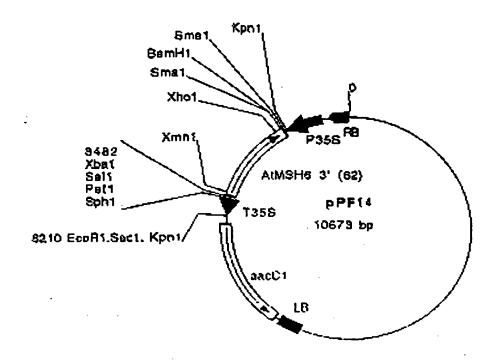


Figure 13

Comments/References: AtMSH6 (S8) 3' side antisens : 62 Sal1/Sal1/T4 (1379bp) into pCW164 BamH1/T4

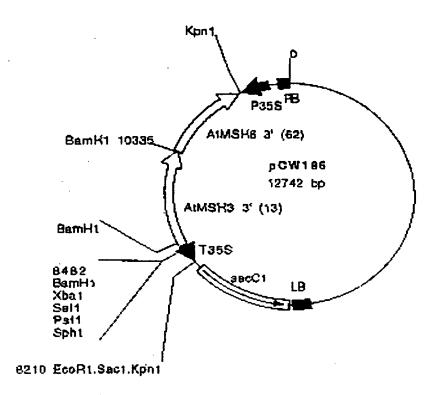


Figure 14

Comments/References: AtMSH8 3'/AtMSH3 3' antisense : AtMSH6 (SB) 3' side (62=1379bp) Salt/Satt/T4 Into pPF13 (pCW184 AtMSH3 (S5) 3' side (19=2104) antisens)/Smat. in LBA4404

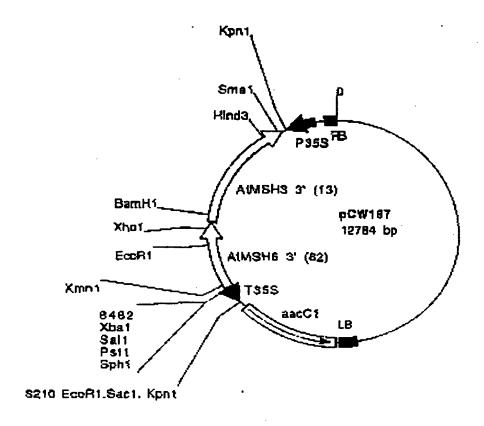


Figure 15

Comments/References: AtMSH3 3'/AtMSH6 3' antisens (0): AtMSH3 (35) 3' eide (13=2104bp) Sal1/Sst1/T4 into pPF14 (AtMSH6 (35) 3'elde (62=1379bp) antisense into pCW164)/Sma1. In LBA4404

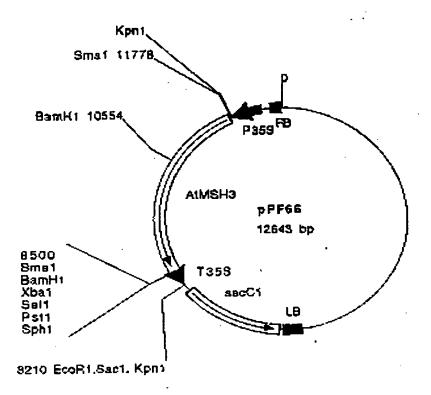


Figure 16

Comments/References: AtMSH3 (SB) complete, sense prientation : pPF26 (3942bp) Email Into pCW164 Small

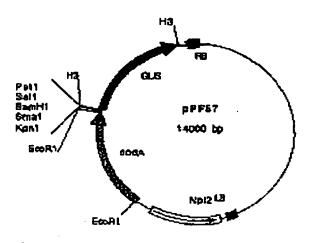


Figure 17

Commente/References: pPZP111 with code EcoR1 casestle in EcoR1 site and HIND GUS casestle in HINDS site. KenR. All genes under Promoter/terminator 35\$

Figure 18

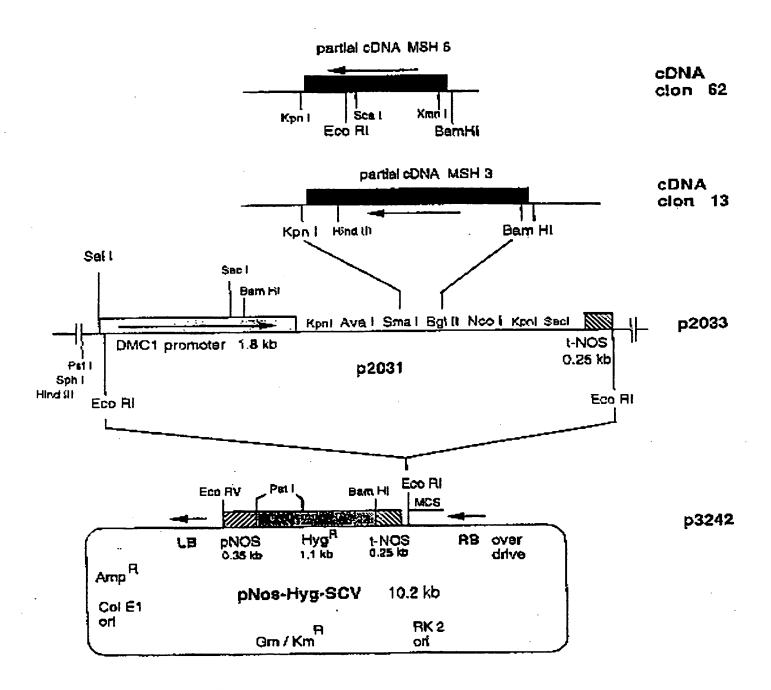
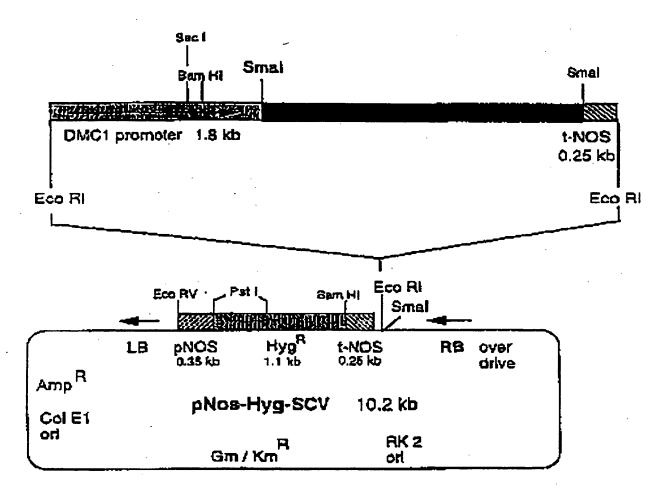


Figure 19

p3243



SEQUENCE LISTING

```
Rhone-Poulenc Agro; Betzner, Andreas Stefan; Doutriaux,
<110>
             Marie-Pascale; Freyssinet, Georges; Perez, Pascual.
<120>
             Methods for obtaining plant varieties
             395498C
<130>
<150>
             PO9745
             1997-10-10
<151>
             98
<1605
<210>
             23
<211>
<212>
             DIVA
<213>
             Artificial sequence.
<220>
             modified_base
<221>
€222%
             11
<223>
             Ţ
<220>
<221>
             modified_base
<222>
             14
<223×
             1
<220>
             modified base
<221>
<222>
             17
             1
<223>
<220>
             Degenerate oligonucleotides UPMU used to isolate AtMSH3 and
<223>
             AtmsH6.
c300>
<301>
             Reenan and Kolodner
<302>
             Genetica
<303>
             132
<306>
             963-973
<307>
             1992
<400>
             1
                                                                         23
ctggatccac nggnecnaay atg
```

<210><211>

<212>

23 DNA

```
<213>
             Artificial sequence
<220>
<221>
             modified_base
<222>
             15
<223>
             1
<220>
             modified_base
<221>
             18
<2223
<223>
             I
<220>
             Degenerate oligonucleotides DOMU used to isolate AtMSH3 and
<223>
             Atmsh6.
<300>
             Reenan and Kolodner
<301>
             Genetics
<3025
<303>
             132
<306>
             963-973
c307>
             1992
<400>
             2
                                                                         23
etggateert ortgogtore raa
<210>
<211>
              24
<212>
             DMA
<213>
             Artificial sequence
<320>
              MSE3 specific primer 636 for PCR using cDNA of Arabidopsis
<223>
              thaliana ecotype Columbia
<400>
              3
                                                                         24
tgctagtgcc tcttgcaage tcat
<210>
              4
              27
<211>
<212>
              DNA
<213>
              Artificial sequence
<220>
              Primer AP1 for PCR using cDNA of Arabidopsis thaliana ecotype
<223>
              Columbia containing adapter sequences ligated to both its
              enda
<400>
```

•	average of the second 27
ccatcctast	acqueteact atagggc 27
<210>	5
<211>	33
<212>	DWA
<213>	Artificial sequence
<220>	
<223>	Primer AP2 for PCR using cDNA of Arabidopsis thalians ecotype
	Columbia containing adapter sequences ligated to both its
	ends
<400>	5
	angetegas and
actractata	gggctcgagc ggc 23
<210>	6
<211×	30
<212>	DNA
<213>	Art).ficial sequence
	•
<220>	
<223>	MSH3 specific primer S525 for PCR using cDNA of Arabidopsis
	thaliana ecotype Columbia
<400>	б
acottetgat	tatgtgtgae gettsaetta 30
23, 3	
<210>	7
<211>	39
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	MEH3 specific primer S51 for PCR using cDNA of Arabidopsis
	thaliana ecotype Columbia
<400>	7
•	
ggatogggta	ctgggttttg agtgtgagg 29
<210>	
<211>	24
<2115 <212>	DNA
<212>	artificial sequents
45173	MICITICIAN SERRONOS
<220>	
<223>	MSH3 specific primer 635 for PCR using cDNA of Arabidopsis
	thaliana ecotype Columbia

	·	
<400>	3	
gracgtgctt	gatggtgttt teac 2	4
<210>	9	
<211>	28	
<212>	DNA	
c213>	Artificíal sequence	
<220>		
<223>	MSH3 specific primer S523 for PCR using cDNA of Arabidops	
(22)	thaliana ecotype Columbia	13
<400>	9	
tcagacagta	tecageatgg cagaagta 2	B
<210>	10	
<211>	33	
¢212>	DNA	
<213>	Artificial seguence	
<220>		
<223>	MSH3 specific primer 1S5 for PCR using cDNA of Arabidopsi thaliana ecotype Columbia	8
₹400>	10	
steergggat	gggeaagcaa aagcagcaga cga 3	3
<210>	11	
<211>	27	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	MSH3 specific primer S53 for PCR using cDNA of Arabidopsi	3
	thaliana ecotype Columbia	
<400>	11	
gacaaagago	gaaatgagge reettgg 2	? 7
<210>	12	
<211>	1250	
<212>	DNA	
<213>	Arabidopsis thaliana ecotype Columbia	
<223>	Clone 52	

<400> 12

cccggg&cgg	дсаадсаваа	gcagcagacg	acttotogtt	tettegetee	CSSACCCSSS	60
terregarte	асдавссдаа	teeggtagee	gaatcatçaa	cacegecace	gaagatatcc	120
gccactgtat	ecttetetee	ttecaagegt	aagcttctct	ccgaccacet	câccāccācā	180
tcacccaata	agcctaaact	Ctotoctoac	octcaaaacc	cagtacccga	tcccaattta	240
caccaaagat	ctccccagag	atttctggsa	ccctcqccgq	aggaatatgt	recegaaaeg	300
ccatcatcga	ggaaatacac	accattggaa	cagcaagtgg	tggagctaaa	gagcaagtac	360
ccagatgtgg	ttttgatggt	ggaagttggt	tacaggtaca	gattettegg	agaagacgcg	420
gagatogcag	cacgcgtgtt	gggtatttac	geteatatgg	atcaceattt	catgacggcg	480
agtgtgccaa	catttegatt	gaausuddat	gtgagaagac	tggtgaatgc	aggatacaag	540
atcggtgcag	сдавусадас	tgaaactgca	gccattaagt	cccatggtgt	aaaccggacc	600
ggccottttt	terggggaet	gtcggpgtlg	tataccaaag	ceaegettga	agcggetgag	660
gatataagtg	gtggttgg	tggtgaagaa	ggttttggtt	cacagagtaa	tttectggtt	720
tgtgt tg t gg	atgagagagt	taaguoggag	acattaggct	gtggtattga	aatgagtttt	790
gatgtt ag ag	toggtättät	tggegttgaa	atttcgaceg	gtgaagetgt	tcatgaageg	. 840
ttcaatgata	actteatgag	aagtggatta	gaggetgtga	ttttgagett	gtcaccagct	900
gagctgttgc	ccggccagcc	tothhoadaa	casactigaga	agtttttggt	ggeacatget	960
ggacctaret	caaacgttcg	agtggaaegt	geeteactgg	attgtttcag	castggtaat	1020
gcagtagatg	aggttatttc	attatgtgaa	aasatcagcg	caggtaactt	agaagatgat	1080
aaagaaatga	ağıtğgəğge	tgetgaaaa	ggsatgtett	gcttgacegt	tcatacaatt	114D
atgaacatgo	cacatrigac	tgttcaagcc	ctegecetaa	egttttgcca	teteaaacag	1200
tttggatttg	aaaggateet	ttaccaaggg	gestrattte	getetttgte		1250

<210> 13 <211> 34 <212> DNA

<213> Artificial asquence

<220>

<223> MSH3 specific primer 255 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

e a no s	13					
attongggtt	aaaatgaaca	agtcggtttt	agtc			34
			•			
<210>	14					_
<211>	27					·
<212>	CNY				•	
<213>	Artificia	l sequence				
<220>	-	•				
	MOUS	ifia avimau		M	12 af 24462	
<223>		ecotype Col		k using cor	A of Arabide	obars
<4DO>	14					
gccacatetg	actgttcaag	ccetege	·		•	27
<210>	15					
<211>	2110					
<212>	DNA		_			
<213>		ils charians	ecotype Co	21 CE013		•
c223>	Clone 13					
<400>	1.5					
gccacatetg	actgttcaag	acetegeeet	aacgttttgc	catotosaac	agtttggart	60
tgaaaggatc	ctttaccaag	gggcctcatt	trgctctttg	teaagtiaca	cagagatgac	120
CEEEEcagee	aatactctgc	aecagttgga	ggttgtgååå	aataattcag	atggatcgga	180
atotggotce	ttattecata	atatgaatca	cacacttaca	gratatggtt.	ceaggettet	240
tagacactgg	gugacucate	ctctatgcga	tagaaattig	statictgeto	ggettgatge	300
tgtttctgag	atttetgett	gcatgggatc	teatagttet	toccagotca	gcagtgagtt	360
ggttgaagaa	ggttetgaga	gagcaattgt	ateacctgag	tittatcicg	tgctctcctc	420
agtettgaca	gctatgtcta	gatcatctga	tattcaacgt	ggaatsacaa	gaatetttea	480
toggactget	asagccacaġ	agttcattgc	agttatggaa	gctattttac	ttgcggggaa	540
gcaaattrag	cggcttggca	taaagcaaga	ctctgaaatg	aggagtatgd	astetgease	600
tgtgcgafct	actettttga	gaaaattgat	ttctgttatt	tcatcccetg	ttgtggttga	£6 0
caatgccgga	assettetet	ctgccctaaa	tazggazgeg	gctgttcgag	gtgacttgct	720
cgacatacta	atcacttcca	gcgaccaatt	teetgagete	gctgaagctc	gccaagcagt	780
tttagtcatc	agggsaaagc	tggattcctc	gatagettea	tttcgcaaga	agcccgctat	840

tegaaatttg	gaatttcttc	aagtgtcggg	gatcacacat	ttgatagagc	tgeecgttga	900
ticcaaggic	cctatgastt	<u>dååtåsøs</u> gt	aaatagcacç	aagaagacta	thegatatea	960
cccccagaa	acagcagetg	gcttggatga	gctagczeta	gcaactgaac	arcttgccac	1020
tgtgaaccga	gettegtggg	ategtttcct	caagagtttc	agtagatact	acacagattt	1080
taaggdtgcc	gttcaagctc	ttgctgcact	ggåctgtttg	cactçccttt	caactctatc	1140
tagaaacaag	aactatgtcc	gtecegagtt	tgtggatgac	tgtgaaccag	ttgagataaa	1200
catacagtct	ggtcgtcatc	ctgtactgga	gactatatta	caagataact	tegteccaaa	1260
tgacacaatt	ttgcatgcag	aaggggaata	rtgccaaatt	atcaccggae	ctaacatggg	1320
aggaaagagc	tgctatatcc	gtcaagttgc	tttaattt.cc	ataatggctc	aggttggttc	1380
otttgt ac ca	gcgtcattcg	ccsagetgea	cgtgcttgat	ggtgttttca	cteggatggg	1440
tgcttcagac	agtatccagc	atggcagaag	tacciticta	gaagaattaa	gtgaagegte	1,500
adacataato	agaacntgit	cttctcgttc	gcttgttata	ttagaugago	trgqaagagg),560
ractageaca	vacgacggtg	nagodatugo	ctatgcaaca	ttacagcatc	toctageaga	1620
aaagagatgt	ttggttettt	ttgtczcgca	ttaccctgaa	atagetgaga	tcagtaacgg	1690
attereaggt	cctgttggga	cataccatgt	ctcgtatctg	acattgcaga	aggataaagg	1740
cagttatgat	catgatgatg	cgacctacct	alotaagett	gtgcgtggto	tttgtagtag	.1900
gagetttggt	tttaaggttg	oteagettge	ccagatacct	ecatcatgta	tacgtcgagc	1860
catttcaatg	gctgcaaaat	tggsagetga	ggcacgcgca	agagagagaa	atacacgcat	1920
д дад аасса	gaaggacatg	aagaaccgag	aggegeagaa	gaatctattt	cggctctagg	1980
tgarttgttt	gcagacctga	aatttgctct	ctctgaagag	gacccttgga	aagcattcga	2040
gtttttaaag	catgettgga	agattgctgg	caaaatcaga	ctaaaaccas	cttgttcstt	2100
ttgacccggg	•		•		•	2110

<210>	16
<211>	2 9
<213>	DNA
<213>	Artificial seguence
<220>	
<223>	MSH3 specific primer S\$1 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400>

adarcadars c	tgggttttg agtgtgagg	2 9
•		
<210>	17	
<311>	30	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	MSH3 specific primer 9525 for PCR using cDNA of Arabidopsis	3
	thaliana erotype Columbia	
<400>	17	
•		
aggitetgat t	atgigigae getttäetta	3 0
•		
c2105	18	
<211>	3522	
<212>	DNA	
c213>	Arabidopsis thaliana ecotype Columbia	
	•	
<220>		
<221>	CDS	
c272>	(100) (3342)	
<223>	AtMSH3 full-length cDNA and deduced sequence of the encoded	i
	polypeptide	
<400>	18	
cctwadasad c	gegogaaaa ttggeaacee asgttegeea tageeacgmo cmegmeette 💎 🙃	0
catttetett a	aacggagga gattacgaat aaagcaatt 9	9
	caa aag cag cag acg att tot ogt tto tto got eee aaa 14	7
Wet Gly Lya	Gln Lys Gln Gln Thr Ile Ser Arg 9he Phe Ala Pro Lys	
1	5 10 15	
ccc asa tcc	eng ant can gaa ong aat ong gta gen gaa tok tok ana 199	5
Pro Lys Ber	Pro Thr His Glu Pro Asn Pro Val Ala Glu Ser Ser Thr	
	20 25 30	
ccà cca cca	aag ata tee gee act gra tee the tet eet tee aag egt 24.	3
Pro Pro Pro	Lys Ile Ser Ala Thr Val Ser Phe Ser Pro Ser Lys Arg	
35	40 45	
aag ott oto	too gae cad dte gee gee geg toa eee aaa aag eet aaa 29	1
Lys Leu Leu	Ser Asp His Leu Ala Ala Ala Ser Pro Lys Lys Pro Lys	
50	55 60	
ctt tet cet	cae act caa aac cea gta eec gat eec aat tta cae caa 333	9
Leu Ser Pro	His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln	
65	70 75 80	

9 .

								S.O.								387
-				_				aca Thr 105		-	-	_				435
								gtg. Val							• •	483
								ysb gsc				_	_	_		531
	-			•		-		cac Xis						_		5 7 9
			•	_				gtg Val	_							627
								Thr 185								675
	-	-						ttt Phe								723
			-	_		_		Ala		_						771
			-					cag Gln	_						-	819
	-		_	_	ràs	_	-	aca Thr			_			_	_	867
-		-	-	_	_			gtt Val 265		-	-		_			915
								gat Asp								963

WO 99/19492 PCT/EP98/05977

						•							
											ggc ggc		1011
											gga Gly		i 0 59
											agc Ser 335		1107
		-	-	_			_	_			agc Ser	_	1155
											gaa Glu		1203
		_	_	-			-		_		cat Kis	_	1251
											ttt Phe		1299
											tca Ser 415		1347
	_	_			_		_		-	_	gag Glu	~	1395
											cat His		1443
											cac Xís		1491
											ctt Leu		1539
						atg Met					tcc Ser 495		1587

													att 11e 510			1635
					•				_	-		_	atg Met		aga Arg	1683
		_											cgg Arg			1731
							_			-			ctt Leu			1779
_			_			-		-		_			atg Met		-	1827
													ttg Leu 590			1875
Val	Ile	Ser 595	Ser	Pro	Val	Val	Val 600	Азр	Ава	Ala	GļĀ	Lya 605	ctt Leu	Гел	Şer	1923
Ala	(.eu 610	neA	Lys	Glu	Ala	Ala 615	Val	Arg	Gly	Asp	620	Leu	Asp	Ile	Leu	1971
11 a 625	The	Ser	Ser	Äsp	630	Phe	Pro	СJи	Гел	Л}а 635	ឧរភ	Ala	Arg	GJD	Ala 640	2019
					_					Ser		2 2	tca 3er		_	2067
													teg Sør 670			2115
		_			_		_	Asp		•	•		atg Kis			2163
		-		_		_	Lys			_		His	Pro			2211

ata Ile 705	Val	g¢t Ala	GJÅ ååc	Etg Lau	gat Asp 710	gag Glu	cca Leu	gct Ala	cta Leu	gca Ala 715	act Thr	gaa Glu	cat Ris	peñ ctt	gcc Ala 720	2259
act Ile	gtg Val	aac Abn	cga Arg	get Ala 725	tog Ser	rgg Trp	Asp gac	agt Ser	ttc Phe 730	rtc Leu	aag Lys	agt Ser	ttc Phe	agt Ser 735	Arg aga	2307
tac Tyr	tac Tyr	aca Thr	gat Asp 740	ttt Phe	aag Lys	gct Ala	gcc Ala	gtt Val 745	caa Gln	g¢t Ala	ctt Leu	gct Ala	gca Ala 750	ctg Leu	gac Asp	2355
tgt Cys	t t g Leu	сас Жів 755	tcc ser	ctt Leu	tca Ser	act Thr	cta Leu 760	tct Ser	aga Arg	aac	aag Lys	aac Asn 765	tat Tyr	gtc Val	egt Arg	2403
ccc Pro	gag Glu 770	Phe	gtg Val	gat Asp	gac Asp	tgt Cys 775	gaa Glu	cca Pro	gtt Val	gag Glju	ata Lie 780	aac Asn	ata Ile	cag Gln	tot Ser	2451
ggt Gly 785	egt Arg	cat His	ect Pro	gra Val	Vao Leu Ctg	gag Glu	act The	ala ile	t ta Leu	caa Gln 795	Y sb geć	vsv	ttr Pbe	gtc Val	eca Pro	2499
aat Asn	gac Asp	aca Thr	acc Ile	ttg Lew 805	cat Ris	aca ala	gaa Glu	9 99 Gly	gna Glu 810	tat Tyr	tga Cys	caa Gln	att Ile	atc 11e 915	ace Thr	2547
gga Oly	cet Pro	aac Asn	atg Met 820	gga Gly	gga Gly	aag Lys	agç Ser	tgc Cys 825	tac Tyr	atc Ile	cgt Arg	cáa Gin	gtt Val 830	Λ)s	tta Leu	2595
tis ell	ccc Ser	ata Ile 835	atg Met	gct Ala	cag Gln	gtt Val	ggc Gly ggc	rcc Ser	Lct Phe	gta Val	cua Pro	grg Ala 845	tca Ser	ttc Phe	gec	2643
aag Lys	ctg Leu 850	cac His	gtg Val	ctt Leu	gat Asp	855 Gly ggt	gtt Val	ttc Phe	açt Thr	Arg ¢gg	atg Met 860	ggt Gly	gct Ala	tca Ser	gac Asp	2691
agt Ser 365	atc	cag Gln	cat Ais	elà aac	aga Arg 870	agt Ser	Thr. scc	ttt Phe	cta Leu	gaa Glu 875	G}u gaæ	tta Leu	agt Ser	gaa Glu	gcg Ala 88D	2739
tca Ser	cac Hia	ata Ile	atc fle	aga Arg 885	acc Thr	tgt Сув	tct Ser	tct Ser	egt Arg 890	tcg Ser	ctt L e u	gtt Val	ata Ile	tta Leu 895	gat gat	2787
gag Glu	ctt Leu	gga Gly	aga Arg	Gly 3gc	act Thr	agc Ser	aca Thr	cac Kis 905	gac Asp	Gly	gta Val	gcc Ala	att Ile 910	gee Ala	tat Tyr	2835

gca aca its dag cat ctd eta gca gaa aag aga igi itig git eti itt Ala Thr Leu Gln His Leu L u Ala Glu Lys Arg Cys Leu Val Leu Phe 915 920 925	2883
gtc acg cat tac ect gam ata get gag atc agt aac gga tte eca ggt Val Thr Ria Tyr Pro Glu Ile Ala Glu Ile Ser Aan Gly Phe Pro Gly 930 935 940	2931
tet get ggg aca tac cat gto tog tat ong aca the cag and gat asa Ser Val Gly Thr Tyr Ris Val Ser Tyr Leu Thr Leu Gln Lys Asp Lys 945 950 955 960	2979
ggc agt tat gat cat gat gtg acc tac cta tat sag ctt gtg cgt Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg 965 970 975	3027
ggt ctt tgc age agg age ttt ggt ttt aag gtt get cag ctt get cag Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Glo Leu Ala Glo 980 985 990	3075
ata cot one how tight at a cight of a god and the ser met Ala Ala Lyb Leu 995 1000 1005	3123
gam got gag gis ogt god aga gag aga aat aca ogo atg gga gad oca Glu Ala Glu Val Arg Ala Arg Glu Arg Ash Thr Arg Met Gly Glu Pro 1810 1015 1020	3171
gas ggs cat gsa gas ceg aga ggc gcs gas gas tet att teg gct cta Glu Gly His Glu Glu Pro Arg Gly Ala Glu Glu Ser Ile Ser Ala Leu 1025 1030 1035 1040	3219
ggt gac ttg ttt gca gae ctg aas htt gch che her qaa gag gae cet Gly Asp Leu Phe Ala Asp Leu Lys Phe Ala Leu Ser Glu Glu Asp Pro 1045 1050 1055	3267
tgg asa goa tto gag ttt tta aag cat got tgg aag att got ggc aaa Trp Lys Ala Phe Glu Phe Leu Lys His Ala Trp Lys Ile Ala Gly Lys 1060 1065 1070	3315
atc aga cta ass ccs set tgt tca ttt tgatttaste ttascattat lle Arg Leu Lys Pro Thr Cys Ser Phe 1075 1080	3362
agcaactges aggtettgat catetgttag ttgegtacta acttatgtgt attagtåtåå	3422
caagaaaaga gaattagaga gatggattet aateeggtgt tgeagtaeat etttteeea	3482
cccccatada abaaaaaaa aabaaaaa aabaaaaaaaaaaaa	3522

<210> 19 <211> 10B1 <312> PRT

~ 6 3.	, , .		MIG	MT 4K	s x ang	s Calc	11191	ia ec	CLYL	<i>y</i> = ∪() T CIUIT	מוכ			
<32	} >		Pol	. урец	ride	: MSE	13								
< 4 0 (0 >		19	•											
Met l	gly	ьуs	Gln	Lу в \$	Oln.	Gln	Thr	Ile	Ser 10	Arg	ррь	Phe	Ala	Pro 15	Lys
Pr ·	Lys	\$et	Pro 20	Thr	Ris	Gји	Pro	ABA 25	Pro	val	Ala	Ğlи	Ser 30	Ser	Tha
Pro	Pro	Pro 35	Lys	lle	Ser	Ala	Thr 40	val	ser	₽ле	Ser	Pro 45	Ser	Lys	Arç
Lys	Նջս 50	Leu	Sor	Азр	His	Leu 55	Ala	Ala	Ala	ser	60 820	rys	Ľув	Pro	Lye
Lau 65	Ser	Pro	Ria	The	Gln 70	ASD	Pro	Va).	БкФ	Asp 75	Pro	Asn	Ļeu	His	G):
Arg	Phe	Leu	C1v	Arg 85	Pine	Leu	Glu	Pro	Ser 90	PY'D	Glu	Glv	тух	Val 95	Pro
Glu	Tier	Ser 	Ser 100	Ser	λrg	ΓÃ2	Tyr	"hr 105	PTO	ren	Glu	Gin	61n 110	Val	Val
Glu	Leu	Lув 115	Ser	Lys	Тут	Pro	Asp 120	Val	Val	Lev	Met	Val 125	Glu	VAl	612
Tyr	Arg 130	Туг	Arg	Phe	Phe	Gly 135	Glu	Asp	Ala	Glu	11e	Ala	Ala	Arg	Va!
Leu 145	Gly	lie	Tyr	Ala	His 150	Mec	Чар	His	Asn	Pbe 155	Met	Thr	ьĺА	Ser	Va] -160
Pro	Thr	Phe	Arg	Leu 165	Asn	Phe	8 注 8	Val	Arg 170	Arg	Leu	Val	aen	Ala 175	Gly
Tyr	Lys	Ile	Gly 190	Val	Val	Lys	Gln	Thr 185	Glu	Thr	Ala	Ala	Ile 190	Lys	Sex
Kis	Gly	Ala 195	aaa	Arg	Thr	Gly	Pro 200	Phe	Phe	Arg	Gly	Leu 205	Ser	Ala	Lei
Tyr	Thr 210	Lys	Ala	Thr	Leu	Glu 215	Ala	Ala	Glu	Asp	11e 220	ser	Gly	Gly	Сує
Gly 225	Glγ	Glu	Glu	Gly	Phe 230	Gly	Ser	Gln	5er	Asn 235	Phe	Leu	Val-	Сув	Va) 24(
raj	Двр	Głu	Arg	Val 245	Lув	ser	Glu	Thr	Lev 250	Gly	Сув	Gly	Ile	Glu 255	Ket

- Ser Phe Asp Val Arg Val Gly Val Val Gly Val Glu Ile Ser Thr Gly 260 250 270
- Glu Val Val Tyr Glu Glu Phe Asn Asp Asn Phe Met Arg Ser Gly Leu 275 280 285
- Glu Ala Val Ile Leu Sor Leu Ser Pro Ala Glu Leu Leu Gly Gin 290 295 300
- Pro Leu Ser Gin Gln Thr Glu Lys Phe Leu Val Ala Met Ala Gly Pro 305 310 315 320
- Thr Ser Asn Val Arg Val Glu Arg Ala Ser Leu Asp Cys Phe Ser Asn 325 330 335
- Gly Ash Ala Val Asp Glu Val Ile Ser Leu Cys Glu Lys Ile Ser Ala 340 345 350
- Gly Ash Len Glu Asp Asp Lys Glu Met Lys Leo Glu Ala Ala Glu Lys 355 360 365
- Cly Met Ser Cya Len Thr Val Eis Thr Ile Met Asn Met Pro Bis Leu 370 375 380
- Thr val Gln Ala Leu Ala Leu Thr Phe Cys His Leu Lys Gln Phe Gly 385 390 395
- Phe Glu Arg Ile Leu Tyr Gln Gly Ala Ser Phe Arg Ser Leu Ser Ser 405 410 415
- Asn Thr Glu Met Thr Leu Ser Ala Asn Thr Leu Gln Gln Leu Glu Val 420 425 430
- Val Lys Asn Asn Ser Asp Gly Ser Glu Scr Gly Ser Leu Phe His Asn 435 440 445
- Met Asn His Thr Leu Thr Val Tyr Gly Ser Arg Leu Leu Arg His Trp 450 460
- Val Thr His Pro Leu Cys Asp Arg Asn Leu Ile Sar Ala Arg Leu Asp 465 470 475 480
- Ala Val Ser Glu Ile Ser Ala Cys Mot Gly Ser His Ser Ser Gln
 485 490 495
- Leu Ser Ser Glu Leu Val Glu Glu Gly Ser Glu Arg Ala Ile Val Ser 500 505 510
- Pro Glu Phe Tyr Leu Val Leu Ser Ser Val Leu Thr Ala Met Ser Arg 515 520 525
- Ser Ser Asp The Gln Arg Gly The Thr Arg The Pha His Arg The Ala

ъуя 545	Ala	ፐከድ	Glu	Phc	11e 550	Ala	val	Met	Glü	Ala 555	Ile	Leu	Leu	ala	Gl ₃ 560
Lys	Gln	Ile	Gln	Arg 565	Leu	Gly	Ile	Ĺуа	Gln 570	Asp	ser	Glu	Met	Arg 575	Sex
Met	Gln	Ser	Ala 580	Thr	val	Arg	\$er	Thr 505	Leu	Leu	Arg	Lys	Leu 590	lle	Sei
٧al	Ile	Ser 595		Pro	Val	٧al	Vа1 600	Asp	neA	Ala	Gly	Lys 605	Leu	Leu	561
Ala	leu 610	Asn	Lys	Glu	Ala	Ala 615	Val	Arg	Gly	Asp	Leu 620	Leu	Asp	Ile	Let
11e 625	Thr	ser	Ser	qzA	630	Phe	Pro	Glu	Lev	Ala 635	Glu	Ala	Arg	Gln	Ala 540
Val	Leu	Val	Ile	Arg 645	G1 u	Lys	Leu	Asp	Ser 650	Ser	I1e	Ala	Ser	Рре 655	Arç
l _i ys	Lys	Leu	660	I)e	Arg	Ash	Letu	665	Phe	Leu	Gln	Val	Ser 670	Gly	Ile
Thr	His	Leu 675	Ile	el#	Leu	Pro	680 089	Asp	ser	rys	Val	Pro 685	H1.S	Asn	Trp
Val	690	Val	Asn	Ser	Thr	Lys 695	Lув	Thr	lle	Arg	Tyr 700	Hib	Pro	Pro	Glı
Ile 705	Val	Ala	GJA	Leu	Asp 710	GIU	Leu	Ala	Leu	Ala 715	Thr	Glu	Нів	Leu	Ala 720
Ile	Val	Asn	Arg	Ala 725	Ser	Trp	Asp	Ser	Phe 730	Lou	Lуs	Ser	Pbe	9er 735	Arg
Tyr	Tyr	Thr	Asp 740	Phe	ГЛя	Ala	Aia	Val 745	Gln	λ la	Ъeп	Ala	Ala 750	Гел	Asg
Cys	Leu	His 755	Ser	Leu	Ser	Thr	leu 760	Ser	Arg	πsa	Lys	Asn 765	Tyr	Val	Arç
Pro	Glบ 770	Phe	Val	ψsp	Asp	Сув 775	Glu	Pro	Val	Glu	11e 780	aeA	I <i>l</i> e	Gln	Sei
Gly 785	Arg	нis	Pro	Val	Leu 790	Glu	Thr	Ile	Leu	Gln 795	Aap	ask	Phe	val	800
λsπ	qaA	Thr	Ile	Leu 805	Hie	Ala	Glu	дју	Glu 810	тут	Сув	Gln	Ile	Ile 315	Thi
Gly	Pro	Asn	Met 820	Gly	Gly	Lys	\$e z	Cya 825	Tyr	Ile	Arg	Gln	Val 830		Leu

- The Ser The Met Ala Glm Val Gly Ser Phe Val Pro Ala Ser Phe Ala 835 840 845
- Lys ten His Val ten Asp Gly Val Phe Thr Arg Met Gly Ala Ser Asp 850 855 860
- Ser lle Gln His Gly Arg Ser Thr Phe Leu Glu Glu Leu Ser Glu Ala 865 870 875 880
- Ser His Ile Ile Arg Thr Cys Ser Ser Arg Ser Leu Val Ile Leu Asp 865 890 895
- Glu Leu Gly Arg Gly Thr Ser Thr His Asp Gly Val Ala Ile Ala Tyr 900 9D5 910
- Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe 915 920 925
- val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Amn Gly Phe Pro Gly 930 940
- Ser Val Gly Thr Tyr His Val Scr Tyr Lew Thr Lew Gln Lys Asp Lyc 945 950 955 960
- Gly Ser Tyr Asp Bis Rep Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg 965 970 975
- Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Gln Leu Ala Gln 980 985 990
- The Pro Pro Ser Cys lie Arg Arg Ala Tie Ser Met Ala Ala Lys Leu 595 1000 1005
- Glu Ala Glu Val Arg Ala Arg Glu Arg Ash Thr Arg Met Gly Glu Pro 1010 1015 1020
- Glu Gly His Glu Glu Pro Arg Gly Ala Glu Glu Ser lle Ser Ala Leu 1025 1030 1035 1040
- Gly Asp Leu Phe Ala Asp Leu Lys Phe Ala Leu Ser Glu Glu Asp Pro 1045 1050 1055
- Trp Lys Ala Phe Glu Phe Leu Lys His Ala Trp Lys Ile Ala Gly Lys 1060 1065 1070
- 11s Arg Leu Lys Pro Thr Cys Ser Phe 1075 1080
- <210> 20
- <211> 24
- <212> DNA
- <213> Artificial sequence

<230>		
<223>	MSH6 specific primer 638 for PCR using cDNA of Arabidopsis thaliana acotype Columbia	
<400>	20	
tototaccag	gegacgasas accg	24
<210>	21	
<211>		
<212>	DNA	
<213>	Artificial sequence	
<220>		
	Twinne Cot for DCD union abid of Anthidoppin thelians again	
c223>	Primer S81 for PCR using cDNA of Arabidopsis thaliana ecoty Columbia	Æ.
<400>	21	
cgtcgccttt	agcatecoot tootteae	28
<210>	22	
<211>	30	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	MSH6 apecific primer 5823 for PCR using cDNA of Arabidopsi thaliana ecotype Columbia	5
<400>	22	
gettggcgca	tctaatagaa tcatgacagg	30
<210>	23	
<211>	24	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	MSK6 specific primer 637 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia	
<400>	23	
gacagegtea	gttcttcaga atgc	24
-2105	24	
<210>	24	

<212>

DNA

<213>	Artificial sequence	
<230×	·	
42232	MSH6 apecific primer ISS for PCR using cDNA of Arabidopsis	
	thaliana ecotype Columbia	
	cuation ecospe cosmuta	
<400×	24	
atecegggat	gcagcgccag agatcgantt tgt	33
<210>	25	
<211>	27	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	MSH6 specific primer SB3 for PCR using cDNA of Arabidopsis	
	thaliana ecotype Columbia	
<400>	25	
ogotatetat	ggetgetteg aattgag	27
<210>	26	
<211>	1385	
<212>	DNA	
<213><223>	Arsbidopsis thalisma ecotype Columbia Clone 43	
· 4433	CIONE 43	
<400>	26	
cccgggatge	agogocagas atosattits tottletter aaaaareeae gyogyegaet	6 0
acgaagggtt	togtttccgg chatgetget ageggegggg geggeagegg aggaecaega 1	20
tttäätgtga	aggaagggga tgctaaaggc gacgctcctg tacgttttgc tgtttcgaaa 1	80
	·	
tetgregatg	aggreagagg aacggatact ccaccggaga aggttccgcg tcgtgtcctg 2	40
ccgtctggat	ttaagorggr tgaatorgre ggtgatgott ogtooctgtt otocaatatt 3	DO
		60
argeacaage	ttgtaaaagt cgatgatega gattgttttg gagagaggag eegagaagat 3	6.
at tate 0000	tarnesses shorotopat obasoaners stankatter ragements	20
gregreeege	tgaatgatto atototatgt atgaaggera atgatgttat tootoaattt 4	
COTECCSATS	atggtamae teamgamaga ameentgett ttmgtttemg tgggmgaget 4	BO
cocanta	ardaranan romadamada marrardere tembessand addamana	-
Qasctagat	cagtagaaga tataggagta gatggcgatg ttcctggtcc agaaacacca 5	40
2		
gggatgcgtc	cacqtqcttc tcgcttgaag cgaqttctgg aggatgaaat gacttttaag 6	00
- -		
	the annutate apparator and a comment to be subtilled annutation to	40

cgeggagaga	agaaagaagt	aescdwscâs	accasatttg	aatggcttga	gtcttctcga	720
atcagggatg	ccastagaag	aogteetgat	gateceettt	acgatagaaa	gaccttacae	780
ataccacctg	atgiciticaa	gaaaatgtcc	gcarcacaaa	agcastattg	gagtgttaag	840
agtgaatata	tggacattgt	gettttettt	aasgtgggga	asttttatga	gctgtatgag	900
ctagatgegg	aattaggtca	caaggagett	gactggaaga	tgaccatgag	tggtgtggga	960
asatgcagae	aggttggtat	ctctgaaagt	gggatagatg	aggcagtgca	aaagctatta	1020
gctegtggat	atasagttgg	acgaatcgag	cagotagaaa	catetgacca	agcāāaagce	1080
agaggtgcta	aractaraat	ccaaggaag	cragttcagg	tattaadted	atcaacagca	1140
agcgagggaa	acategggcc	tgatgccqtc	catettettg	ctacasasga	gatcaamatg	1200
gagctacaee	agtgttcaac	tgtgtatgga	tttgcttttg	ttgactgtgc	tgeettgagg	1260
ttttgggttg	ggtcratcag	cqacqarçcə	teatgtgetg	cccttggage	gttattgatg	1320
caggettete	caaaggaagt	gttatarzác	agcaaaggge	tatemagaga	agcacaaaag	1380
gctctaagga	aatatacgtt	deceddarcc	acggrggcac	agttggctcc	agtaccacsa	1440
gtaatggggg	atacagatge	tgetggagtt	agaaatataa	tagaatotaa	cggatacttt	1500
aaaggetett	crgaatcatg	gaactgcgct	gttgatggtc	taaatgaatg	tgatgttgcc	1560
cttägtgete	ttggagaget	asttaatcat	ctgtctaggc	taaagctaga	agatgtactt	1620
aagcatgggg	atatttttcc	ataccaaget	tacaggggtt	georgagaat	cgatggccag	1580
acgatggtaa	atcttgagat	atttaacaac	agctgtgatg	gtggtectta	agggaccttg	1740
taceaatate	ttgatametg	tgttagteca	actggtaage	gactottaag	gaattggatc	1800
tgccatccac	tcsaagatgt	agaaagcatc	aataaacggc	ttgatgtagt	tgaagaattc	1860
acggcaaact	cagaaagtat	gcasstcact	ggccagtate	tocacaaact	tccagactta	1920
gaaagactgc	toggaegeat	caagtotago	gttogatoat	cagcetetgt	gttgcctgct	1980
cttctgggga	aaaaagtgct	gaaacaacga	gtraaagcat	ttgggcaaat	tgtgaaaggg	2040
ttcagaagtg	gaattgatct	gttgrrggct	ctacagaagg	aaccaaacat	gatgagtttg	2100
ctctataaac	totgtaaact	tcctatatta	gtaggaaaaa	gcgggctaga	gttatttctt	2160
tetcaatteg	&&GC&GCCAL	agatageo				2188

<210>	27
<212>	1305
<212>	DNA
<213>	Arabidopsis thaliana ecotype Columbia
<223>	Clone 62
s400a	27

catcasecte tgtgttgcet getettetgg ggaaak&Agt getgaaac&& cgagtta&ag 60 -cattleggea aattetgaaa gegtteagaa gtggaattga tetgttgttg getetaeaga 120 aggaatcaaa tatgatgagt ttgctttata aactotgtaa acttcccata tcagtaggaa 180 aaagogggot agagttatti ottiotoaat togaagoago catagatago gactttocaa 240 attatcagaa ccaagatgtg acagatgaaa acgotgaaac totcacaata ottatcgaac 300 360 tttttatega aagageaact caatggtetg aggteattea caccataage egcetagatg tectgagate coetgeaare geageaagte tetetgetgg aageatggee aggeetgtma 420 ttttteeega ateagaaget aeagateaga ateaghaaac muaagggeea ataettaaaa 480 torsaggact acgerators titigoagoog cagergatigs teastiffeet gittergaatig 540 600 atatactoot tggogagget agaagaagca gtggoagcat toatootogg toatbyttac ់ឥ៩០ tgacgggacc asacatgggc ggassatcsa otettettet tgcaacatgt ctggccgtta tettigeera actiggetge taegigeegi gigaqielig egaaatetee etegiggata 720 780 ctaccetcae aaggestgge geatebgata gaateacgae aggagagagt acctttttgg tagastgrac tgagacageg tcagttette agaatgebac tcaggattea ctagtaatee 840 900 ttgåcgaact gggcagagga actagtactt tcgatggata cgccattgca tactcggttt 960 CCGGCCACCE ggtagagaaa gttcaatgtc ggatgctctt tgccaccacat taccaccete teaccaagga attegegtet cacceaegtg teacctegaa acacatgget tgegeattea 1020 1080 aatcaagato tgattatoaa ocaogtggtt gtgatcaaga cotagtgtto ttgtaccgtt taaccgaggg agottgtoot gagagotaog gadttoaagt ggcactcatg gottggaatac 1140 caaaccaagt ggttgaaaca gcatcaggtg ctgctcaagc catgaagaga tcaattgggg 1200 1260 addaCttCAA gtcaagtgag Ctaagatctg agttotcaag totgcatgaa gactggctca agreatiggt gggtatitet cgagtegeec acaacaatge ecceatigge gaagatgact 1320 acqueettt gttttgetta tggeatgaga teaaateete ttactgtgtt cecaaataae 1390

ccggg	1385
<210>	28
c211>	34
<212>	DNA
<213>	Arrificial sequence
	Meeting and and and
<220>	
<223≻	MSH6 specific primer 288 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia
<400>	26
ateregggtt	atttgggåå¢ acagtaagag gatt 34
<210>	29
<211>	27
<212>	DNA
<213>	Artificial sequence
	•
<220>	
<233>	MSH6 specific primer SB2 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia
<400>	29
gcgttcgatc	ateageetet gtgttg: 27
<210>	30
<211>	3606
<212>	DNA
<213>	Arabidopsis thaliana ecotype Columbia
<220>	-
<221>	CDS
<222>	(142) (3468)
<223>	AtMSH6 full-length cDNA and deduced sequence of the encoded polypeptids
<400>	30
aaagttgag	ccetgaggag tatcgtttec gecattteta egacgcaagg cgaaaatttt 60
tggcgccaat	ctttccccc tttcgaatte tctcagctea aaacatcgtt tetctctcsc 120
teteteteae	Adttecasas A atg cag ege cag aga teg att ttg tet tte 171 Met Gln Arg Gln Arg Ser lle Leu Ser Phe

														99¢ Gly 25		573
														gtg Val		257
														teg Şer		315
														gtt Val		363
ogt Arg 75	cgt Arg	gtc Val	ctg Leu	ccg Pro	tct Ser 80	eja 339	ttt Phe	aag Lys	ecg Pro	gct Ala 85	gaa Glu	tee Ser	gcc	gst Gly	gat Asp 90	411
														gtc Val 105		459
gac Asp	yzâ câa	gat Aep	110 CAs F3f	tct Ser	gga Gly	gag Glu	yr.d sdd	agc Ser 115	Arg	gaa Glu	gac Asp	gtt Val	gtt Val 120	eeg Pro	ctg Leu	507
aat Asn	увр	toa Ser 125	Ser	cca Leu	tgt Cys	atg Met	130 Lys	Ala	aat Asn	gat. Asp	ger Val	att Ile 135	Pro	caa Gln	ttt Phe	555
		Asn					Gln					Ala		agt Ser		603
	Gly					Arg					Ile			gat Asp	ggc Gly 170	651
					Glu					Arg					Arg ege	699
ttg Leu	asg Lys	cga	gtt Val 190	Leu	Glu Glu	gat Asp	gaa Glu	atg Met 195	Thr	ttt Phe	.aag :Lys	gag Glu	gat Asp 200	aag Lye	gtt Val	747
ect Pro	gta Val	teu 205	Asp	tct Ser	aac Asa	aaa Lys	370 9x0 935	, Leu	aaa Lys	acg Met	cte Lev	cag Glr 215	Ast	ceg	gtt Val	795

tot	gga	cao	aaa	222	722	ar-		~	~~~			+++		t aa	 +	943
											ьув 230					743
gag Glu 235	tct Ser	trt Ser	ega	ace Ile	agg Arg 240	yab gar	gec Ala	aat naA	aga Arg	aga Arg 245	cgt Arg	cct Pro	gat Asp	gat Asp	ecc Pro 250	891
											gat Asp					939
											aag Lys					987
							_				tat Tyr		•			1035
			-				_			•	310 11p	_	_		_	1003
											tct Şer					1131
									_		tat Tyr		_			1179
		_		_			_		_		gcc Ala	_		_		1227
											act Thr					1275
											ctt Leu 390				aaa Lye	1323
											gtg Val					1371
											ggg Gly					1419

gac Asp	gca Ala	tca Ser	tgt Cys 430	gct Ala	got Ala	ctt Leu	GJ y gga	gcg Ala 435	tta Leu	ttg Leu	atg Met	cag Gln	gtt Val 440	tct Ser	eca Pro	1467
Lys 2ag	Ċ]π Ġ9\$	gtg Val 445	tta Leu	taC Tyr	gac Asp	agt Ser	ааа 1ув 450	eja 888	cta Leu	tça Ser	aga Arģ	gaā Ģlu 455	gca Ala	caa Gln	aag Lys	1515
								gjà ĉaĝ								1563
cca Pro 475	gtā Val	cca Pro	caa Gln	gta Val	atg Met 430	Gly ggg	gat Asp	aca Thr	gat Aвр	gct Ala 485	gct	GľÅ ââσ	gtt Val	aga Ar g	aat Asn 490	1611
								aaa Lys								1659
								Cys Cys						λla		1707
g ga Gly	Glu gag	cta Leu 525	lle	aat Asn	cat His	ren C£3	tol Ser 530	yrg	cta Leu	aag Lys	cta	gaa Glu 535	Asp	gtå Val	ent. Leu	1755
aag Lys	cat His 540	6J À 243	даt	att 11e	ttt Phe	cca Pro 545	.ያአェ	caa Gln	gtt Val	tac Tyr	адд Ухд 550	Gly	Cys	ctc Leu	yr d aga	1803
att Tle 555	Asp	gjy gge	Gln	aog Thr	atg Met 560	Val	aat	cc: Lev	gag Glu	ata Ile 565	5pe	аас Авл	aat Asn	ago Ser	сус Сув 570	1851
gat Asp	ggt Gly	GJĀ	cct Oro	tca Ser 575	Gly	acc Thr	ttg Leu	tac Tyr	aaa Lys 580	2 la	Ctt Lev	gat Asp	aac Ast	tgt Cya 585	· Val	1899
agt Ger	cca Pro	act Thr	ggt Gly 590	. TAs	.yrd	ctc Leu	tta Lev	agg Arg S95	Авл	tgg Trp	ato Ile	tgc Cya	600 600	Pro	ctc Leu	1947
aas Lys	gat Asp	gta Val 605	. Glu	ago Sei	ato	aat Asn	aaa Lys 610	: Arg	ctt Lev	gat Asp	gça Val	gtt Val 619	Glı	gaa Glu	ttc Phe	1995
acg Thi	gça : Ala : 620	Asr	tca Ser	gađ Glu	ı agt	atg Net 625	: Ġļī	ato lle	act Thi	gg¢ Gly	cag (Gl) 63(ואב ו	cto Lev	cac His	aaa Lys	2043

ctt	cca	gac	tta	gaa	aga	ctg	ctc	ada	ege	atc	aag	tet	age	gtt	cga	2	2091
635	Pro	двА	Leu	Glu	97.d 94.0	Leu	Leu	Gly	Arg	fle 645	L :ye	Ser	Ser	Val	Arg 650		
tca Ser	tca Ser	grc Ala	tct Ser	gtg Val	teg Lev	cct Pro	A) a	ctt Leu	ctg Leu	gja ààà	aaz Lys	aaa Lys	gtg Val	ctg Leu	aaa Lys	2	139
				655					660					665			
			Lys	gca Ala				11e								2	2187
			670					675					680				
		Leu		ttg Leu												2	235
		683					690					695					
ctt Leu	Tyr	Lya	cr c Leu	tgt Cys	aaa Lys	Гęл	cct Pro	ata Ile	tta Leu	gta Val	Gly	aaa Lys	agc Ser	gjå 232	cta Leu	2	283
	700					705					711						-
ខា្រ				tct Ser												2	2331
715					720					725		٠			730		
				caa Glp												2	2379
				735					740					745			
				ctt Lev												2	2427
			750					755				·	760				
				≥gc Ser'												â	2475
		765					770			···· 5		775					
				gct Ala												2	2523
-1124	780			,,,,,	G1,	785	rac	~10	n A	710	790	.116	PIRE	PLU	GIU		
tca	gas gas	gct	aca	gat Asp	csa	Bat	cag	aga	a ca	aaa	333	CCR	ata	ctt	aaa	2	2571
795	316	nia		veħ	800	ROII	GIR	nys	1134	B05	GIA	PID	116	гел	870 FAR		
ate	caa	gga	cta	tgg	cat	CCE	ttt	gca	gtt	gca	gcc	gat	990	CRA	ttg	. 3	8619
116	GIN	OLY	reu	Trp 815	ліЅ	ETO	rn5	WIB	850 A91	WT 9	WT5	авр	цίλ	G1n 825	Г е л		
cet	gtt	crg	aat	gat	ata	cte	ctt	gge	gag	get	aga	aga	agc	agt	ggc	2	667
110	144	FTO	830	QZ A	TIG	ren	Teg	61 y 835	GIU	WIW	arg	arg	Ser	Ser	Gly		

agc Ser	att Lle	cat Ris 945	ect Pro	¢gg Arg	tca Ser	ctg Leu	tca Leu 950	ctg Leu	acg Thr	gga Gly	cca Pro	aac Aan 855	atg Met	gg¢ Gly	gga Gly	2715
aaa Lyg	tca Ser 860	act Thr	ctt Leu	ctt Leu	egt. Arg	gca Ala 865	aca Thr	tgt Cys	l∕s ii ctg	gcc Ala	gtt Val 870	atc I)e	ttt Phe	gcc	caa Gln	2763
ctt Leu 875	gg¢ Gly	tgc Cys	tac Tyr	gtg Val	ccg Pro 800	tgt Cyв	gag	tet Ser	cye	gaa Glu 885	atc Ile	rcc Ser	ctc Leu	gtg Val	gat Asp 890	3811
act Thr	atc Ile	ttc Phe	aca Thr	agg Arg 895	ctt Leu	gjy ggc	gca Ala	cct Ser	gat Asp 900	aga Arg	atc Ile	atg Mat	aca Thr	gga 905	gag Glu	2859
agt Ser	acc Thr	ctt Phe	ttg Leu 910	gta Val	Gj <i>n</i> gas	tgc Çya	act Thr	gag Glu 915	aca Thr	gcg Ala	tca Şer	gtt Val	ett Leu 920	cag Gln	aat Asn	2907
gca Ala	act Thr	cag Gln 925	gat Asp	tca Ser	cta Leu	gta Väì	acc Ile 930	ert Leu	gac	GJu Gaa	reg sev	935 Gly Ggc	yrd	gjy Sga	act Thr	2955
agt Şer	act Thr 940	Phe	gat Asp	gga Gly	cac Tyr	gcc Ala 945	IJ¢	gca Ala	tac Tyr	teg Sev	gat Val 950	БуБ	ogt Arg	cac His	ren Grâ	3003
gta Val 955	GJ <i>n</i> 393	aaa Lys	gtt Val	caa Gln	tgt Cys 960	Arg	atg Met	at.c Leu	ttt Phe	gca Ala 965	The.	cat His	tac Tyr	cac His	970	3051
cto Leu	acc Thr	Lye	gaa Glu	ttc Phe 975	Ala	tct Ser	cac His	cca Pro	egs Arg	V&l	ecc Thr	teg Ser	aza Lye	cac His 985	atg : Met	3099
gct Ala	tgc Cys	gça Ala	ttc Phe 390	Lys	tca Sex	, ¥tâ sās	tct Ser	995 Aeb gat	туч	caa Gln	red Pro	cgt Arg	ggt Gly	′ Сув	gat Asp	3147
Cln	gac	cta Leu 1005	val	ttc Phe	ctg Led	tac Tyr	cgt Arg	Leu	acc Thr	gag Glu	. Gly gga	gct Ala	Cys	cet Pro	Glu Gag	3195
Ser	tac Tyr 1020	Gly	ctt Lev	caa Glm	gtg Val	gea Ala 1025	Lev	: atg Met	gct Ala	gga Gly	ata / 11e	Pro	aad Asr	cae	a gtg 1 Val	3243
gtt Val 103	Glı	acs Thr	ges Als	tes Ser	ggt : Gly	/ Ala	gct Ala	caa Gla	gco Ala	e ato a Met 1049	: Lys	yas ga	a tea g Sea	a att	999 Gly 1050	3291

gga	aac	ttc	aag	Сcа	aqt	gaÿ	cta	aga	tet	DSD	tte	tca	agt	cts	cat	3339
Glu	Asn	Phe	Lys	Ser	Ser	Glv	ьеи	Arg	ser	Glu	Phe	Sex	ser	ren	His	
			:	1055					1060					1065		
	A	F ~ ~	at a													
Glas	gac Aen	rgg	Levi	aag	CCA	ttg	<u>gr3</u>	ggt	att	tct	cga	gtc	gec	cac	aac	3387
Giu	HSP	111	1070	PÅR	zer	Lev			ITB	Ser	Arg			His	Asn	
			10,0					1075					1080			
aat	acc	ccc	att	aac	gaa	gat	gae	tac	gac	act	ttn	+++	tac	++-	t oa	3435
ABD	Āla	Pro	Ile	Gly	Glu	Asp	Asp	TVr	Tab	Thr	Levi	Dhe	Cyp	Len	52D	2422
		1085		,			1090	-1-	1102			1095	-y-	₽ ∈0	45.5	
cat	gag	atc	aaa	rcc	tct	tac	tgt	gtt	ccc	888	taa	atgg	cta			3478
		Ile	Lys	ser		Tyr	САЗ	Val	Pro	Lya						
	1100					1105										
			at at							_						
tgai	a t a	aca I	CLAC	rtga	ag ci	ccgti	caag	CE	cctg	cctc	tet	gatg	ttt i	arte	ctcct	à 3538
aaaa	aato	ett i	stata	at caa	3 25 212	137.L.C	<u>.</u>		enar:		33.35				AAAAA	. 7550
	9								oguc.	, watt	atta	aaaa	ada (aaaa4	AAAAA	a 3598
282	BEGE	De C														3606
						1										
	_															
<210			31													
<211			110													
<213			PR													
<223						೯ ರಗಿತ	41191	78 C	COLAL	> ₩ (((シエ パしの)1A				
			200	Imar		. MCL	I C									
~~~	<b>5</b> >		501	) Abei	)tide	MS}	<b>{ 6</b>		•							
< 401			20. 31	) ÀD∈ì	tide	MS)	<b>{</b> 6									
				l Abei	etide	MS}	<b>{</b> 6		-							
<400	)>	Arg	31										Pro	Thr	Ala	
<400	)>	Arg	31			: MS}							Pro	Thr 15	Ala	
<400 Met	l> Gln		31 Gln	Arg 5	Ser	lle	Ŀеи	Ser	Phe 10	Phe	Gln	Lув		15		
<400 Met	l> Gln		31 Gln Lys	Arg 5	Ser		Ŀеи	Ser	Phe 10	Phe	Gln	Lув		15		
<400 Met	l> Gln		31 Gln	Arg 5	Ser	lle	Ŀеи	Ser	Phe 10	Phe	Gln	Lув		15		
<400 Met 1 Ala	l> Gln Thr	Thr	31 Gln Lys 20	Arg 5 Gly	Ser Leu	ile Val	Leu Ser	Ser Gly 25	Phe 10	Phe Ala	Cln Ala	Lув Ser	Gly	15 Gly	Gly	
<400 Met 1 Ala	l> Gln Thr	Thr Gly	31 Gln Lys 20	Arg 5 Gly	Ser Leu	lle	Leu Ser Asp	Ser Gly 25	Phe 10	Phe Ala	Cln Ala	Lys Ser Aap	Gly	15 Gly	Gly	
<400 Met 1 Ala	l> Gln Thr	Thr	31 Gln Lys 20	Arg 5 Gly	Ser Leu	ile Val	Leu Ser	Ser Gly 25	Phe 10	Phe Ala	Cln Ala	Lув Ser	Gly	15 Gly	Gly	
<400 Met 1 Ala Gly	dln Thr	Thr Gly 35	31 Gln Lys 20 Gly	Arg 5 Gly Pro	Ser Leu Arg	Ile Val Phe	Leu Ser Asn 40	Ser Gly 25 Val	Phe 10 Asp Arg	Phe Ala Glu	Gln , Ala Gly	Lys Ser Asp 45	Gly 30 Ala	15 Gly <b>Ly</b> s	Gly	
<400 Met 1 Ala Gly	Gln Thr Ser	Thr Gly 35	31 Gln Lys 20 Gly	Arg 5 Gly Pro	Ser Leu Arg	ile val Phe	Leu Ser Asn 40	Ser Gly 25 Val	Phe 10 Asp Arg	Phe Ala Glu	Gln Ala Gly Val	Lys Ser Asp 45	Gly 30 Ala	15 Gly <b>Ly</b> s	Gly	
<400 Met 1 Ala Gly	dln Thr	Thr Gly 35	31 Gln Lys 20 Gly	Arg 5 Gly Pro	Ser Leu Arg	Ile Val Phe	Leu Ser Asn 40	Ser Gly 25 Val	Phe 10 Asp Arg	Phe Ala Glu	Gln , Ala Gly	Lys Ser Asp 45	Gly 30 Ala	15 Gly <b>Ly</b> s	Gly	
< 400 Met 1 Ala Gly Asp	Gln Thr Ser Ala	Thr Gly 35 Ser	31 Gln Lys 20 Gly Val	Arg 5 Gly Pro	Ser Leu Arg Phe	Ile Val Phe Ala 55	Leu Ser Asn 40 Val	Ser Gly 25 Val	Phe 10 Asp Arg	Phe Ala Glu Ser	Gln Ala Gly Val	Lys Ser Asp 45	Gly 30 Ala Glu	15 Gly Lys Val	gly Gly	
< 400 Met 1 Ala Gly Asp	Gln Thr Ser Ala	Thr Gly 35 Ser	31 Gln Lys 20 Gly Val	Arg 5 Gly Pro	Ser Leu Arg Phe	ile val Phe	Leu Ser Asn 40 Val	Ser Gly 25 Val	Phe 10 Asp Arg	Phe Ala Glu Ser	Gln Ala Gly Val	Lys Ser Asp 45	Gly 30 Ala Glu	15 Gly Lys Val	Gly Gly Arg	
<400 Met 1 Ala Gly Asp	Gln Thr Ser Ala	Thr Gly 35 Ser	31 Gln Lys 20 Gly Val	Arg 5 Gly Pro	Ser Leu Arg Phe	Ile Val Phe Ala 55	Leu Ser Asn 40 Val	Ser Gly 25 Val	Phe 10 Asp Arg	Phe Ala Glu Ser	Gln Ala Gly Val	Lys Ser Asp 45	Gly 30 Ala Glu	15 Gly Lys Val	gly Gly	
<400 Met 1 Ala Gly Asp 65	oln Thr Ser Ala 50	Thr Gly 35 Ser	31 Gln Lys 20 Gly Val	Arg 5 Gly Pro Arg	Ser Leu Arg Phe Pro 70	Tle Val Phe Ala 55	Leu Ser Asn 40 Val	Ser Gly 25 Val Ser	Phe 10 Asp Arg Lys	Phe Ala Glu Ser Arg 75	Gln Ala Gly Val 60	Lys Ser Asp 45 Asp	Gly 30 Ala Glu Leu	15 Gly Lys Val	Gly Mrg Ser 80	
<400 Met 1 Ala Gly Asp 65	oln Thr Ser Ala 50	Thr Gly 35 Ser	31 Gln Lys 20 Gly Val	Arg 5 Gly Pro Arg	Ser Leu Arg Phe Pro 70	Ile Val Phe Ala 55	Leu Ser Asn 40 Val	Ser Gly 25 Val Ser	Phe 10 Asp Arg Lys	Phe Ala Glu Ser Arg 75	Gln Ala Gly Val 60	Lys Ser Asp 45 Asp	Gly 30 Ala Glu Leu	15 Gly Lys Val	Gly Mrg Ser	
<400 Met 1 Ala Gly Asp 65 Gly	Gln Thr Ser Ala 50 Thr	Thr Gly 35 Ser Asp	31 Gln Lys 20 Gly Val Thr	Arg Sly Pro Arg Pro Ala 85	Ser Leu Arg Phe Pro 70 Glu	Ile Val Phe Ala 55 Glu Ser	Leu Ser Asn 40 Val Lys	Ser Gly 25 Val Ser Val	Phe 10 Asp Arg Pro Asp 90	Phe Ala Glu Ser Arg 75	Gln Ala Gly Val 60 Arg	Lys Ser Asp 45 Asp	Gly 30 Ala Glu Leu	15 Gly Lys Val Pro	Gly Arg Ser 80	
<400 Met 1 Ala Gly Asp 65 Gly	Gln Thr Ser Ala 50 Thr	Thr Gly 35 Ser Asp	31 Gln Lys 20 Gly Val Thr Pro	Arg Sly Pro Arg Pro Ala 85	Ser Leu Arg Phe Pro 70 Glu	Tle Val Phe Ala 55	Leu Ser Asn 40 Val Lys	Ser Gly 25 Val Ser Val	Phe 10 Asp Arg Pro Asp 90	Phe Ala Glu Ser Arg 75	Gln Ala Gly Val 60 Arg	Lys Ser Asp 45 Asp	Gly 30 Ala Glu Leu	15 Gly Lys Val Pro	Gly Arg Ser 80	
<pre>&lt; 400 Met     1 Ala Gly Asp Gly 65 Gly</pre>	Gln Thr Ser Ala 50 Thr	Thr Gly 35 Ser Asp	31 Gln Lys 20 Gly Val Thr	Arg Sly Pro Arg Pro Ala 85	Ser Leu Arg Phe Pro 70 Glu	Ile Val Phe Ala 55 Glu Ser	Leu Ser Asn 40 Val Lys	Ser Gly 25 Val Ser Val	Phe 10 Asp Arg Pro Asp 90	Phe Ala Glu Ser Arg 75	Gln Ala Gly Val 60 Arg	Lys Ser Asp 45 Asp	Gly 30 Ala Glu Leu	15 Gly Lys Val Pro	Gly Arg Ser 80	
<400 Met 1 Ala Gly Asp 65 Gly Asn	ola Thr Ser Ala 50 Thr Phe	Thr Gly 35 Ser Asp Lys	31 Gln Lys 20 Gly Val Thr Pro His 100	Arg Sly Pro Arg Pro Ala 85	Ser Leu Arg Phe Pro 70 Glu Phe	Ile Val Phe Ala 55 Glu Ser Val	Leu Ser Asn 40 Val Lys	Ser Gly 25 Val Ber Val Gly Val 105	Phe 10 Asp Arg Lys Pro Asp	Phe Ala Glu Ser Arg 75 Ala	Gln Ala Gly Val 60 Arg Ser	Lys Ser Asp 45 Asp Val	Gly JO Ala Glu Leu Cys 110	15 Gly Lys Val Pro Phe 95 Ser	Gly Gly Arg Ser GO	
<400 Met 1 Ala Gly Asp 65 Gly Asn	ola Thr Ser Ala 50 Thr Phe	Thr Gly 35 Ser Asp Lys	31 Gln Lys 20 Gly Val Thr Pro His 100	Arg Sly Pro Arg Pro Ala 85	Ser Leu Arg Phe Pro 70 Glu Phe	Ile Val Phe Ala 55 Glu Ser	Leu Ser Asn 40 Val Lys	Ser Gly 25 Val Ber Val Gly Val 105	Phe 10 Asp Arg Lys Pro Asp	Phe Ala Glu Ser Arg 75 Ala	Gln Ala Gly Val 60 Arg Ser	Lys Ser Asp 45 Asp Val	Gly JO Ala Glu Leu Cys 110	15 Gly Lys Val Pro Phe 95 Ser	Gly Gly Arg Ser GO	

Met Lys Ala Asn Asp Val Ile Pro Gln Phe Arg Ser Asn Asn Gly Lys 135 130 Thr Sin Glu Arg Ash His Ala Phe Ser Phe Ser Gly Arg Ala Glu Leu 150 195 145 Arg Ser val Glu Asp Ile Gly Val Asp Gly Asp Val Pro Gly Pro Glu 17D Thr Pro Gly Met Arg Pro Arg Ala Ser Arg Leu Lys Arg Val Leu Glu 185 Asp Glu Met Thr Phe Lys Glu Asp Lys Val Pro Val Leu Asp Ser Asn 195 Lys Arg Leu Lys Met Leu Gla Asp Pro Val Cys Gly Glu Lys Lys Glu 215 Wal Asn Glu Gly Thr Lys Phe Giu Trp Lou Clu Sor Ser Arg Ile Arg 230 235 Asp Ala Ash arg Arg Arg Pro Asp Asp Pro Leu Tyr Asp Arg Lys Thr 250 255 245 Lou Bis The Pro Pro Asp Val Phe Lys Lys Met Ser Ala Scr Gln Lys 265 260 Glp Tyr Trp Ser Val Lys Ser Glu Tyr Met Asp Ile Val Leu Phe Phe Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu Leu Asp Ala Glu Leu Gly His Lys Glu Lou Asp Trp Lys Met Thr Met Sor Gly Val Gly Lys Cys 310 315 305 Arg Gln Val Gly Ile Ser Glu Ser Gly Ile Asp Glu Ala Val Gln Lys 325 33D Leu Leu Ala Arg Gly Tyr Lys Val Gly Arg Ile Glu Gln Leu Glu Thr 345 Ser Asp Cin Ala Lys Ala Arg Cly Ala Asn Thr Ile Ile Pro Arg Lys 355 360 Leu Val Glm Val Leu Thr Pro Ser Thr Ala Ser Glu Gly Asn Ile Gly 375 3 B Q 370 Pro Asp Ala Val His Leu Leu Ala Ile Lys Glu Ile Lys Met Glu Leu 395 390 Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala Phe Val Asp Cys Ala Ala

- Leu Arg Phe Trp val Gly Ser lie Ser Asp Asp Ala Ser Cys Ala Ala 420 425 430
- Leu Gly Ala Leu Leu Met Gln Val Ser Pro Lys Glu Val Leu Tyr Asp 435 440 445
- Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys Ala Leu Arg Lys Tyr Thr 450 455 460
- Leu Thr Gly Ser Thr Ala Val Gin Leu Ala Pro Val Pro Gin Val Met 465 470 475 480
- Gly Asp Thr Asp Ala Ala Gly Val Arg Asn Ile Ile Glu Ser Asn Gly
  485 490 495
- Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn Cys Ala Val Asp Gly Leu 500 505 510
- Asn Glu Cys Asp Val Ala Lou Ser Ala Leu Gly Glu Leu Ile Asn His 515 520 525
- Leu Ser Arg Leo Lys Leo Giu Asp Val Leo Lys His Gly Asp The Phe 530 535 540
- Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg Ile Asp Gly Gln Thr Met 545 550 555 560
- Val Asn Leu Glu Ile Phe Asn Asn Ser Cys Asp Gly Gly Pro Ser Gly 565 570 575
- The Leu Tyr Lys Tyr Leu Asp Asn Cys Val Ser Pro The Gly Lys Arg
- Leu Leu Arg Asn Tro Ile Cys Ris Pro Leu Lys Asp Val Glu Ser Ile 595 600 605
- Asn Lys Arg Leu Asp Val Val Glu Glu Phe Thr Ala Asn Ser Glu Ser 610 620
- Met Gln Ile Thr Gly Gln Tyr Leu His Lys Leu Pro Asp Leu Glu Arg 625 630 635 640
- Let Let Gly Arg Ile Lys Ser Ger Val Arg Ser Ser Ala Ser Val Let 645 650 655
- Pro Ala Leu Leu Gly Lys Lys Val Leu Lys Gln Arg Val Lys Ala Phe 660 665 670
- Gly Gln Ile Val Lys Gly Phe Arg Ser Gly Il Asp Leu Leu Ala 675 680 585
- Leu Gln Lys Glu Ser Aan Met Net Ser Leu Leu Tyr Lys Leu Cys Lys 690 595 700

STOCIO--WO GOLGAGOATTI

- Leu Pro Ile Leu Val Gly Lys Ser Gly Leu Glu Leu Phe Leu Ser Gln 705 710 715 720
- Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro Asm Tyr Cln Asm Glm Asp 725 730 735
- Val Thr Asp Glu Asn Ala Glu Thr Leu Thr Ile Leu Ile Glu Leu Phe 740 745 750
- Ile Glu Arg Ala Thr Gln Trp Ser Glu Val Ile His Thr Ile Ser Cys 755 760 765
- Leu Asp Val Leu Arg Ser Phe Ala Ile Ala Ala Ser Leu Ser Ala Gly
  770 775 780
- Ser Met Ala Arg Pro Val Ile Phe Pro Glu Ser Glu Ala Thr Asp Glu 785 790 795 800
- Ann Glm Lys Thr Lys Gly Pro Tie Leu Lys Ile Glm Gly Leu Trp Mis 805 810 815
- Pro Pho Ala Val Ala Ala Asp Sly Glm Leu Pro Val Pro Asm Asp Ile 820 825 830
- Let Let Gly Glu Ala Arg Arg Ser Ser Gly Ser Ile His Pro Arg Ser 835 840 845
- Leu Leu teu Thr Gly Pro Asn Met Gly Cly Lys Ser Thr Leu Leu Arg
- Ala Thr Cys Leu Ala Val Ile Phe Ala Gln Leu Gly Cys Tyr Val Pro 865 870 875 880
- Cys Glu Ser Cys Glu Ile Ser Leu Val Asp Thr Ile Phe Thr Arg Leu 885 890 895
- Gly Ala Ser Asp Arg Ile Met Thr Gly Glu Ser Thr Phe Leu Val Glu 900 905 910
- Cys Thr Glu Thr Ala Ser Val Leu Gln Asn Ala Thr Gln Asp Ser Leu 915 920 925
- Val Ile Leu Asp Glu Leu Gly Arg Gly Thr Ser Thr Phe Asp Gly Tyr 930 935 940
- Ala Ile Ala Tyr Ser Val Phe Arg His Leu Val Glu Lys Val Gln Cys 945 950 955 960
- Arg Met Leu Phe Ala Thr His Tyr His Pro Leu Thr Lys Glu Phe Ala 965 970 975
- Ser Ris Pro Arg Val Thr Ser Lys His Met Ala Cys Ala Phe Lys Ser 980 985 990

Arg Ser Asp 1 995	Tyr Gln Pro Arg Gly Cys Asp Sln Asp Leu Val Phe Leu 1000 100\$	
Tyr Arg Leu 7	Thr Glu Gly Ala Cys Pro Glu Sex Tyr Gly Leu Gln Val 1015 1020	
Ala Leu Mot i 1025	Ala Gly Ile Pro Asn Gln Val Val Glu Thr Ala Ser Gly 1030 1035 1040	
Ala Ala Gln A	Ala Met Lys Arg Ser lle Gly Glu Asn Phe Lys Ser Ser 1045 1050 1055	
	Ser Glo Phe Ser Ser Leo His Glo Asp Trp Leo Lys Sor 1065 1070	
Leu Val Gly 1075	lle Ser Arg Val Ala His Asn Amn Ala Pro Ile Gly Glu 1080 1085	
Asp Asp Tyr / 1090	Asp Thr Lau Phe Cys Lett Trp His Glu Ile Lys Ser Ser 1095 1100	
Tyr Cys Val 1 1105	Pro lys	
<210>	32	
<211>	24	
<212>	CNA	
<213>	Artificial sequence	
<220>		
<223>	Forward primer for PCR amplification of ATRGENEA microsatellite	
<400>	32	
accatgoata g	cttaaactt cttg	24
<210>	33	
<211>	22	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Reverse primer for PCR amplification of ATHGENEA microsatellite	
<400>	33	
acataaccac a	aataggggt ¢C	22

<210.5	34				
<211>	18				
4212×	cna				
<213×	Artificial sequence	•			
<220>					
<223>	Forward primer DMCIN-A for PCR on getthaliana ssp. Landsberg eracta *Ler		DNA	of.	Arabidopsis
<400>	34				
gaagogatat	tqttcgtg		•		18
<210>	35				
_					
<211>	19				
<212>	DNA				
<213>	Artificial sequence				
<220>					
<223×	Reverse primer DMCIN-B for PCR on go thaliana ssp. Landsberg erecta "Ler		DNA	of	Arabidopaia
<400>	35	•			
agattocoag	aacattcc				18
<210>	36				
<211>	31				
<212>	DNA				
<213>	Artificial sequence				
<320>					
<223>	Forward primer DMCIN-1 for PCR on go thaliana ssp. Landaberg erecta "Ler		DNA	of	Arabidopsis
<400>	36		•		
acgcgtcgac	tcagctatga gattactcgt q		•		31.
<210>	37				
<211>	29				
<212>	DNA				
<213>	Artificial sequence				
<220>		-			
c273>	Reverse primer DMCIN-2 for PCR on grantaliana ssp. Landsberg erecta "Ler		DNA	of	Arabidopsis
<400>	37			٠	
getetagate	tetegeteta agactetet				29

<210×	3 <b>8</b>
<211>	32
<212>	DNA
<213×	Artificial sequence
<220>	
<233>	Forward primer DMCIN-3 for PCR on genomic DNA of Arabidopsi thaliana sap. Landsberg erecta "Ler"
<400>	38
gétetagagé	ttctcttaag taagtgattg at • 3
<210>	39
<211>	48
<212:	DNA
<233>	Artificial sequence
<2205	
<223>	Reverse primer DMCIN-4 for PCR on genomic DNA of Arabidopsi chaliana sep. Landsberg erecta "Ler"
<400>	39
receceggge	trgagagate tecatggiti circagerer atquatec 4
<210>	40
<2115	26
<2125	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer DMC1a for PCR on genomic DNA of Arabidopeis theliana ssp. Landsberg erects "Ler"
<400>	40
acgcgtcgac	gaattegeaa gtgggg 2
<210>	41
<211>	38
<212>	DNA
<213>	Artificial seguence
<220>	
<223>	Reverse primer DMC1b for PCR on genomic DNA of Arabidopsis thalians ssp. Landsberg erecta "Ler"
<400>	41

nccatggaga	tetecegggt acceatetge ttcgaggg	8
<210>	42	
<212>	20	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Forward primer for PCR amplification of ATBAT1 SSLP marker Arabidopsis thaliana subapecies	in
<400>	42	•
gecactgegt	geatgatatg 2	0
<210>	43	
<211>	22	
<212>	DNA	
<313>	Artificial Bequence	
(813)	MILITICIBI BEGINANIA	
<220>	·	
<223>	Reverse primer for PCR amplification of ATEAT1 SSLP marker Arabidopsis thaliana subspecies	in
<400>	43	
cgaacageca	acattaattc cc 2	2
<210>	44	
<211>	18	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Forward primer for PCR amplification of NGA63 SSLP marker i	D
	Arabidopsis thaliana subspecies	
<400>	44	
aaccaaggca	cagaagcg	. 8
-27 n -		
<210>	45	
<211>	18	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Reverse primer for PCR amplification of NGA63 SSLP marker i Arabidopsis thalians subspecies	n

38

< 400>	45	
acccaagtga	togopace	. 18
		·
<210>	46	
<211>	21	
<213>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Forward primer for PCR amplification of NGA24 Arabidopsis thaliana subspecies	8 SSLP marker in
<400>	46	
taccyaacca	asacacsaag g	21
<210>	47	
<211>	22	
<212>	DNA	
<2135	Artificial sequence	
55433	Alliterar Bequeite	
<220>		
<223>	Reverse primer for PCR amplification of NGA24 Arabidopsis thaliana subspecies	8 SSLP marker in
<400>	47	
totgtatete	ggtgaattet cc	22
- 73 4-	<b>48</b>	
<210>		
c2115	22	
<212><213>	DNA	
<213>	Artificial sequence	
<220>	•	
<223>	Forward primer for PCR amplification of NGA12 Arabidopsis thalisms subspecies	8 SSLP marker i
<400>	48	,
ggtctgttga	Cgtcgtaagt cg	22
<210>	49	
<211>	22	
<312>	DNA	
<213>	Artificial sequence	
~ <b>~ ~ ~</b> ~ ~	TO CAR S COM BE SMENICE	
<220>		

<223>	Reverse primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thalians subspecies
<400>	4.9
atottgaaac c	tttagggag gg 22
<210>	50
<211>	22
<212>	DNA
<213>	Artificial sequence
	•
<220>	
<223>	Forward primer for PCR amplification of NGA280 SSLP marker in Arabidopsis thaliana subspecies
<400>	50
ctgatctcac g	gacaatagr gc 22
<210>	51
<211>	20
<212>	DNA
<213>	Artificial sequence
,	
<22D>	
<223>	Reverse primer for PCR amplification of NGA280 SSLP marker in
	Arabidopsis thaliana subspecies
<400>	51
ggotocataa a	aagcgcacc 20
<210>	<b>52</b> .
<211>	21
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Porward primer for PCR amplification of NGAll1 SSLP marker in
	Arabidopsis thaliana subspecies
.400-	
<\$00>	52
ctccagtigg a	agctanagg g 21
c210>	53
<211>	21
<212>	DRA
<213>	Artificial sequence

<220>		
<223>	Reverse primer for PCR amplification of NGA111 SSLP marker 1:	n
	Arabidopsis thaliana subspecies	
<400>	53	
+m++ <b>+</b> +++>	g gacaaatgge g 21	
cycecees	3 3000000330 3	
٠		
<210>	<b>54</b>	
<211>	20	
<213>	DNA	
<213>	Artificial sequence	
<220>	5 1 1 5 mm 1141 1 mm 2 mm 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
<233>	Forward primer for PCR amplification of NGA168 SSLP marker is	Ü
	Arabidopsis thaliana subspecies	
<400>	54	
ccttcacat	c caaaacccsc 20	,
<210>	55	
<311>	20	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Reverse primer for PCR amplification of NGA168 BSLP marker 1	<b>)</b>
~~~	Arabidopais thaliana subspecies	•
•	ALGOLOGICA CALLEDIA GUNDIO COCO	
<40D>	55	
gcatataccı	r acaaccagaa 20	J
<210>	56	
<211>	20	
<212>	DNA	
<213>	Artificial sequence	
-4207	ALLIACIAL DEGRESSO	
<220>		
<223>	Forward primer for PCR amplification of NGA1126 SSLP marker	
	in Arabidopsis thaliana subspecies	
<400>	56	
_		_
cgctacgct	t ttoggtasag 20)

<210>	57	
<211>	20	
< 212 >	UNA	
<2135	Artificial sequence	
	• '	
<220>		
€223>	Reverse primer for PCR amplification of NGA1126 SSLP marker	
	in Arabidopsis chalians subspecies	
<400>	57	
goacagtoca a	TERRAPE.	o
		v
<210>	58	
<211>	20	
<212>	DNA	
<213>		
<812>	Artificial sequence	
<2 20 >		
	December 1 man 1 m	
<223>	Forward primer for PCR amplification of NGA361 SSLP marker	ענ
	Arabidopsis Chuliana subspecies	
<400>	58	
		_
aaagagatga g	aatttögse	P
<210>	59	
<211>	23	
<212>	DNA	
<213>	Artificial sequence	
<22D>		
<223>	Reverse primer for PCR amplification of NGA361 SSLP marker	in
	Arabidopsis thaliana subspecies	
<400>	59	
acatatcaar a	attaaagt agc 2	:3
	•	
<210>	60	
<211>	16	
<212>	DNA	
<213>	Artificial sequence	
•		
<220>		
<223>	Forward primer for PCR amplification of NGA168 SSLP marker	מב
	Arabidopsis thaliana subspeci s	
	•	
<400>	60	

ccátctactà	cactgeeg 18
<210>	61
<211>	32
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of NGA168 SSLP marker in Arabidopsis thaliana subspecies
<400>	61
gaggacatgt	ataggageet eg
<210>	63
<211>	20
<212×	DNA
<213>	Artificial sequence
<220>	
<223>	Porward primer for PCR amplification of AthBIO2 SSL2 marker in Arabidopsis thaliana subspecies
<400>	62
tgacctcccc	ttecarggag 20
<210>	63
<211>	22
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of AthBIO2 SSLP marker in Arabidopsis thaliana subspecies
<400>	63
ttaacagaaa	cccaaagett te 22
<210>	64
<211>	21
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Porward primer for PCR amplification of AthURIQUE SSLP market in Arabidopsis thaliana subspecies

,4 400 5	64
aggcaaatgt	coattteatt g 21
<210>	65
<211>	20
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of AthUBIQUE SSLP marker in Arabidopsis thaliana subspecies
<400>	65
acgacatggc	agatttetee 20
<210>	66
<211>	21
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer for PCR amplification of NGA172 SSLP marker in Arabidopsis thaliana subspecies
<400>	66
ag ctgc tcc	ttatagegte e 21
<210>	67
<211>	19
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of NGA172 SSLP marker in Arabidopsis thaliana subspecies
<400>	67
catoogaatg	crattgttc 19
<210>	68
<211>	68 21
<212>	DNA
<213>	Artificial sequence
•	
<220>	

< 223 >	Forward primer for PCR amplification of NGA136 SSLP marker in Arabidopsis chaliana subspecies
<400 >	58
gaaaaacgc	tactttcgtg g
<210>	69
<211>	22
c212>	DNA
<213>	Artificial sequence
c220»	
<223>	Reverse primer for PCR amplification of NGA126 SSLP marker in Arabidopsis thalisms subspecies
<400>	69
caagagcaat	atcaagagea ge 22
<210×	79
<211>	29
<212>	DNA
<213>	Arcificial sequence
<220>	
<223>	Forward primer for PCR amplification of NGA162 SSLP marker is Arabidopsis thaliana subspecies
<400>	70
catgomattt	geatcugagg 20
<210>	71
<211>	22
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of NGA162 SSLP marker 1
	Arabidopsis thaliana subspecies
<400>	71
ctctgtcact	ettteetet gg 22
<210>	72
<211>	21
<212>	ANG
<213>	Artificial sequence

<220>	•	
<333>	forward primer for PCR amplification of NGA6 SSLP marker : Arabidopsis thaliana subspecies	in
<400>	72	
tggatttett (cetetettea e	21
	•	
<210>	73	
<311>	21	
<212>	DNA	
<213>	Artificial sequence	
	•	
<220>		
<223>	Reverse primer for PCR amplification of NGA6 SSLP marker : Arabidopsis thaliana subspecies	in
<400>	73	
atggagasuc '	ttacactgat c	21
<210>	74	
<211>	20	
<2125	DNA	
<213>	Artificial sequence	
42132	ALLIE TOTAL Baguence	
<228×		
<2235	Forward primer for PCR amplification of NGA12 SSLP marker	in
	Arabidopsis thaliana subspecies	
<400>	74	
	••	
aatgttgtcc	teceeteete	20
<210>	75	
<211>	22	
<212>	DNA	
<213>	Artificial sequence	
	UT DIETOTHY DOGODING	
<220>		
<223>	Reverse primer for PCR amplification of NGA12 SSLP marker	in
	Arabidopsis thaliana subspecies	
<400>	75	
	•	

<210>	76
<211>	- 21
<212>	DNA
<213>	Artificial sequence
	•
<530>	
<223>	Forward primer for PCR amplification of NGA8 SSLP marker in
	Arabidopsis thaliana subspecies
<400>	76
gaggcasat	ctttatiteg g
•	
<210>	77
<211>	22
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of NGA8 SSLP marker in
	Arabidopsis chaliand subspecies
<400>	
<40D>	77
rääcttreäs	ttatasacat cc 22
<210>	78
c211>	21
<212>	DNA
<213>	Artificial sequence
	wrpiiioigi pedmence
<220>	
<223>	Forward primer for PCR amplification of NGA1107 SSLP marker
	in Arabidopsis thaliana subspecies
	*** **********************************
<400>	78
goganaasac (AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
	21
•	
<210>	79
<211>	21
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of NGA1107 SSLP marker
	in Arabidopsis thaliana subspecies
	· · · · · · · · · · · · · · · · · · ·
<400>	79

cdatâ#sccd	acagaattag g	21
<210>	8 C	
<211>	21	
<212>	DNA	
<213>	Artificial sequence	
	Madifiated degreeate	
<220>		
<223>	Forward primer for PCR amplification of NGA225 SSLP market Arabidopsis thaliana subspecies	r in
<400>	80	٠
gaeatccaaa	tcccagagag g	21
<210>	B1	
<211>	22	
<212>	DNA	
<213>	Artificial Bequence	
<220>		
<223>	Develope aginer for Day and let	_
(263)	Reverse primer for PCR amplification of NGA225 SSLP marker Arabidopsis theliana subspecies	. in
<400>	81	
totocccact ;	agttttgtgt cc	22
<210>	B2	
<211>	19	
c212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Forward primer for PCR amplification of NGA249 SSLP marker Arabidopsis thaliana subspecies	: in
<400>	62	
taccgtcaat :	teategee	19
		•
c210s	B3	
<211>	22	
<212s	AND	
<213>	Artificial sequence	
-336-		
<220> <223>	Communication of the communica	
· .	Reverse primar for PCR amplification of NGA249 SSLP marker Arabidopsis thaliana subspecies	·in

48

<400×	83
ggatococtas	ctgtasaatc cc
<210>	84
<211>	22
₹212>	DNA
<213>	Artificial sequence
<220>	
<223>	Porward primer for PCR amplification of CA72 SSLP marker in Arabidopsis thaliana subspecies
<400>	84
eatcccagta	accaaacaca ca 22
<210>	85
<211>	20
<212>	DNA .
<213>	Arnificial sequence
(223)	war transplace wednesde
<220>	
<223>	Reverse primer for PCR amplification of CA72 SSLP marker in Arabidopsis challanz subspecies
<400>	85
cccagtctsa (ecangancan 20
<210>	RG
<2115	20
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Rotward primar for PCP analisianian as ways and
	Forward primer for PCR amplification of NGA151 SSLP marker in Arabidopsis thaliana subspecies
<400>	86
gttttgggaa g	ıttitgetgg 20
<210>	87
<211>	24
<212>	DNA
<213>	Artificial sequence
<220>	

«223»	Reverse primer for PCR amplification of NGA151 SSLP marker in Arabidopsis thaliana subspectes
×400>	67
cagtictadas g	cgagagtat gatg 24
<210>	B8 .
<211>	27
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Porward primer for PCR amplification of NGA106 SSLP marker in Arabidopsis thaliana subspecies
<400>	88
gttałggagt t	tctagggea eg 22
<21 0 >	. 89
<211>	20
. <212>	DNA
<213>	Artificial sequence
<230>	
<223 »	Reverse primer for PCR amplification of NGA106 SSLP marker in Arabidopsis thaliana subspecies
<400>	B9
tgccccaret t	gttettete 20
<210>	90
<311>	20
<212>	DNA ~
<213>	Artificial sequence
<220>	
<223>	Forward primer for PCR amplification of NGA139 SSLP marker in
	Arabidopsis thalians subspecies
<400>	90
agagotacca g	gateegatgg 20
<210>	91
<211>	21
<212>	DNA
<213>	Artificial sequence

<220>		
<223>	Reverse primer for PCR amplification of NGA139 SSLP marker Arabidopais thaliana subspecies	: ir
<400>	91	
ggtttcgttt	cactatecag g	21
<210>	92	
<211>	22	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Forward primer for PCR amplification of NGA76 SSLP marker Arabidopsis thaliana subspecies	πż
<400>	92	
ggagaaaatg	tcactctcca cc	22
22.0		
<210>	93	
<211> <212>	20	
<213>	DNA Artificial sequence	
<220>		
<223>	Reverse primer for PCR amplification of NGA76 SSLP marker Arabidopsis thaliana subspecies	in
<400>	93	
aggcatçgga	gacatttacg	20
<210>	94	
<211>	20	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Forward primer for PCR amplification of ATHSO191 ESEP mark in Arabidopsis thaliana subspecies	er
<400>	94	
ctccaccaat	Catgossatg	20

<210>	95
<211>	21
<212×	DNA
c213>	Artificial Bequence
c220>	,
<233>	Reverse primer for PCR amplification of ATHSO191 SSLP marker in Arabidopsis thaliana subspecies
<400>	95
tgatgttgat	ggagatggtc a 21
<210>	96
c211>	22
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Forward primer for PCR amplification of NGA129 SSLP marker in Arabidopsis thaliana subspecies
<400>	96
tcaggaggaa	ctaaagtgag gg 22
<210>	97
<211>	22
<212>	DNA
<213>	Artificial sequence
<220>	
<223>	Reverse primer for PCR amplification of NGA129 SSLP marker in Arabidopsis thaliana subspecies
<400>	97
cacactgaag	atggtettga gg 22
<210>	98
<211>	8062
<212>	DNA
<213>	Arabidopsis thaliana ecotype Columbia
<220>	
<223>	Ganomic DNA sequence of AtMSR6
<400>	97
ztttttggtt	get acaata aaggtatace gttttatete ateaatataa étatatataa 60

aagaaasgaa	ayatatatat	tgtttttcca	tttatcaaac	662553666	gastttttt	120
ttacttttta	cattggteaa	ra saa tacaa	gatasacgac	accesttaat	catttcccaa	190
ttttacccet	aagtttaaca	cctagaacct	tctccatctt	egczageaea	gcctgattag	240
gaecagcttt	accattetca	tatteetgaa	ctacctgagt	cetetrattg	atctgtttcg	300
ccasatccgc	ttgtgacatc	ttottotoca	atctcgctct	cognatoato	aacctcacct	360
ctgctttcac	acgatecate	accacadant	etgittette	ttccagette	tecgtgttaa	420
tcacoggaac	cgccgtagat	ttcccctttt	tgttcgaacc	ggcatcgaat	ttettaaccg	480
tttgaaccgc	gacacegttt	ctcagagctg	ogttaacege	ttteggateg	cgtaggtett	54D
ggctettttg	ttttgatttg	tggagaacta	ctggttccca	gtettgtgtt	actgctcctg	600
ggtatctgct	cggcatcqtc	gatgasttga	gagaaagqaa	саасдстава	ättttattaa	660
tetgagettt	gaaattgaga	aacgatgaaq	atgaagaatg	ttgttgagag	gattqtgata	720
tttatacəta	cgaagattgg	tttctggaga	attegateat	crettectec	attttcgtct	780
ctggaacgtt	cttagagatg	attgacgacg	tgtcattate	rgatttgcag	ttaaccmatg	840
ctttttgggt	tggattcgtg	gtacaccata	ttatccgatc	tggctcaatg	gttttätata	900
aatteggete	toggtteggt	tatgagttat	Cattaeaatt	aagetaacea	aaaattttcg	960
taaaatttat	tteggtttea	attoggator	cttacttcca	gaaccgaatt	attegaaace	1020
adaderadee	gaaccgaata	ccsatgcccg	attgactcgc	tggotagaaa	gatccaacgg	1080
tateceatea	tagaacatas	atcggacggt	cateaaagee	tcaaagagtg	sacagtcasc	1140
ammaaaagtt	gagccctgag	gagtatogtt	teegocattt	ctacgacgea	aggcgaaaat	1200
ttttggcgcc	aatettteec	ccctttcgaa	tteteteage	tcaaaacatc	gtttetetet	1260
CBStStStStSt	cacaattcca	aaaaatgcag	cgccagagat	cgattttgtc	tttcctccaa	1320
asacccacgg	cggcgactac	gmagggtttg	gtttccggcg	atgetgetag	ç3 GÇG GGGGE	1380
adcødcådø 3	accacgattt	aatgtgaagg	aaggggatgc	caaaggcgac	gcttctgtac	1440
gttttgctgt	ttcgaaatct	gtcgatgagg	ttagaggaac	ggatacteca	ccddedaadd	1500
tteegegteg	tgtcctgccg	tctggattta	agccggctga	atcegceggt	gatgettegt	1560
ccctgttctc	caatattatg	cataagtttg	taaaagtega	tgatogagat	tgttctggag	1620
agaggtecta	atottogatt	ctcttaattt	tgttatettt	agetggaaga	agaagatteg	7680

tgtaatttgt	tgtattcgtt	ggagagatte	tgattactgc	sttggatogt	rgretacasa	1740
tittcaggag	cogagaagat	gttgttccgc	tgaatgattc	atototatgt	atgaaggeta	1800
atgatgttat	teetraattt	cgttccaaca	atggtaaaac	tcaagaaaga	aaccatgctt	1860
ttagrttcag	tgggagaget	gaacttagat	cagtagaaga	tateggagta	gatggcgatg	1920
ctcatggtec	agaaacacca	dada racare	cacgtgotte	tegettgaag	cgagttctgg	1980
aggatgaaat	gacttttaag	gaggataagg	ttretgtatt	ggactetaac	aaaaggctga	2040
aaatgctcca	ggatccggtt	tgtggagaga	agaaagaagt	asacgasoga	accaaatttg	2100
aatggettga	gtettetega	atcagggatg	ccsatagaag	Acgrectigat	gatcecettt	2160
acgatagaaa	gaccttacac	ataccacctg	atgttttcaa	gamaatgtot	gcatcacasa	2220
egcaatattg	gagtgttaag	agtgaatata	tggacattgt	getttettt	aaagtggtta	2280
gtaactatta	atctagtgtt	caatccatct	cctcaatgcg	atttgttcac	ttacatotgt	2340
ttacgttatg	CtCttCtCag	gggaaatttt	atgagotgta	tgagctagat	gcggaattag	2400
gtcacaagga	gcttgactgg	sagacgaeca	tgagtggtgt	gggaaaatgc	agacaggtaa	2460
attagttgaa	acaactggcc	tgottgaatt	attgtgtcta	taaattttga	caccaccttt	2520
tgtttcaggt	tggtatetet	d sse &£ddds	tagatgaggc	agtgcaaaag	ctattagete	2580
araaaraada	gaaccatcat	actttatgga	attegtttac	tgctacttcg	gctaggattt	2640
aagaaatggs	aatcacttca	agcatcatta	gttaggatcc	tgagaactca	ggatgttttc	3700
ttättegtta	tataataagt	cttttcatca	aggagteace	aacaaaactt	gcacaatatt	2750
tgtgtgctca	ctggcaaggr	atatatacco	agctaacctt	tgctagttca	ctgtagtaac	2820
agttacggat	aacatatgtt	tactrgtarg	tggtaccetc	attitgtctc	tcatggaggc	2880
tttcaagcct	tgtgttgasa	ctggacagtt	acatatgott	ccascagaas	ctagcatgca	2940
gattcatatg	ctttcctatt	ctactaatta	tgtattgaca	cactegttgt	ttettttgaa	3000
agatataaag	ttggacgaat	egagcagcta	gaaacatetg	accaagcaaa	agccagaggt	3060
gctaataetg	taagttttct	tggataggtc	<u> </u>	ttgcagaetg	tttttgatca	3120
tttcttttc	tgtacattac	tttcatgctg	taattaactc	aatggctatt	ctggtctgat	3180
tatcaga ta a	Ccccaaggaa	gctagttcag	gtattaactc	catcaacagc	aagegaggga	3240
aacatogggc	ctgatgedet	contottett	gctataaaag	Agenticitiz	tttacktakt	3300

tatettatea	tgttcagttc	Atccangtcc	tgasssetta	cactottott	taecastett	3360
ccatcaaget	gtytaaagga	tttggaatta	gaaaatcatt	atttgatgct	ttgttttata	3420
tgcaagaggt	tcccttgaaa	agacotgiti	aagatt¢ttt	gcacttgaaa	anticaatct	3480
ttttaagtga	stcrectact	ttcttacaat	gatcatagtc	tgcsattgca	tgtcmagtma	3540
tatcattect	tgttactgca	tecepetett	tcttaatgac	cattgtctat	gttgtgtttg	3600
tetegtgtge	tggagaaaat	gatagotgat	ccaagetgta	cattatcatg	attaagtagr	3660
tgct caggaa	ttgcccttgg	ttacattgee	taatggtttg	atgtcaattt	ttcttctgea	3720
tctttattt	agatcaasat	ggagctacaa	aagtgttcaa	ctgtgtatgg	atttgctttc	3780
gttgactgtg	ctgccttgag	gttttgggtt	gggtccatca	gcgatgatgc	atcatgtgct	3840
getettggag	cgttattgat	gcaggtaagc	aagtgtattc	tgtatcttat	gtgtaccatg	3900
tgacttcctg	tgcstatatt	tääättäcag	gaactaattc	tgaateseea	tttggtatgt	3960
tttttccagg	tttrtcraea	ggaagtgtta	tatgacagra	aaggtaaact	gettgtateg	4020
ccagttgttt	tgttasacag	aatstaaggt	aaatgacact	ggttaattta	aagtgcatac	4080
atgttgaeat	attgcagggc	tatcaagaga	agcacaaaag	gototaagga	aatatacgtt	4140
gacaggtacc	atttcagtag	gcasgctsac	tgacaattta	acegeteace	gaatgatagg	4200
totottaaac	Attgttaatg	tagatgatgt	ttatgtttca	atctaatagg	gtctacggcg	4250
gtacagctgg	ctccagtacc	acaagtaatg	ggga tacag	atgetgetgg	agttagaast	4320
ataatayaat	ctaacggata	ctttaaaggt	tottorgaat	catggaactg	tgctgttgat	4380
ggtctaaatg	aatgtgatgt	tgreettagt	gctcttggag	agctaättaa	toatotgtot	4440
aggetaaagg	tgtgtrggct	tgtttagttt	ttgcttttca	Caaattaagc	aaaggaactt	4500
ttcstaactt	acagtttcta	tctacttyca	gctagaagat	gtacttaagc	atggggatat	4560
ttttccatac	caagtttaca	ggggttgtct	cagaattgat	ggccagacga	tggtasatct	4620
tgagatattt	Bacaatagct	gtgatggtgg	teetteagge	aagcgcatat	ttcttttttg	4680
ataacetcaa	ctagagggca	gacatagaag	gaaeeattct	aatacttcgt	acggatetee	4740
agtazgtəat	agcogatttt	tgtttaccta	tgtagggacc	ttgtacaaat	atcttgatas	4800
ctgtgttagt	ccaactggta	gegactett	aaggaattgg	atctgocatc	cactcamega	4860
t gtagaaagc	accaa t aaac	ggcttgatgt	agttgaagaa	ttcacggcaa	actcagaaag	4920

tatgcaaatc	aceggecage	atctccacaa	acttocagac	tragaaagac	cacreadera	4320
catcaagtet	agcgttcgat	catcagcold	tgtgttgcct	getettetgg	ggaaaaaagt	5040
gctgaaacaa	cgagtaagta	tcastcacas	gttttetgag	taatgrette	catgagtagt	5100
acaggactaa	aacattacgg	gtotagotaa	agactgttct	ccttcttttg	caatgtctgg	5160
ttattcatta	catttetett	aacttattgc	attg caggtt	assgcatttg	ggcaaattgt	5220
gaaagggttc	agzagtggaa	ttgatctgtt	gtrggeteta	cagaaggaat	caaatatgat	5280
gagttegett	tatasactct	gtaaacttee	tatattagta	agasassadca	ggetagagtt	5340
arttettter	caattcgaag	cagccataga	tagegacttt	ccaaattatc	aggtgcccat	5400
ctatctttca	tacettacaa	caaaatgtct	gtcactactc	aaagcaatge	atatggctta	546D
gateteaact	cacaccccga	ggatcctaaa	gggatttgct	ttttattcct	astytttttg	5520
gatggtttga	tttatttcta	acttgaactt	attaatettg	taccagaacc	aagatgtgac	5580
agatgaaaac	gctgaaactc	tcacaatact	tatcgaactt	tttatogaaa	gagcaactca	5640
acggrotgag	gtcattcaca	rcataagetg	cctagatgtc	ctgagatctt	ttgcaatcgc	5700
agcaagtctc	tetgetggaa	geatggecag	gcctgttatt	tttcccgaat	cagaagetae	5760
agatcagaat	cagaasacas	aagggccaat	acttaaaatc	caaggactat	ggcatccatt	5820
tgcagttgca	gccgatggtc	aattgeetgt	tocgaatgat	atactccttg	gcgaggctag	5880
aagaagcägt	ggcagcattc	atecteggte	attgttæctg	асдддассаа	acatāāācāā	5940
aaaatcaact	cttottcgtg	caacatgtct	ggecgttate	tttgcccaag	tttgtatact	6000
cgttagetaa	ttactctatt	ctttgcaatc	agttcttcaa	catgaataat	aaattotgtt	6060
tratgtatga	agcttggctg	ctacgtgccg	tgrgagtett	gcgaaatctc	cctcgtggat	6120
actatettea	caaggcttgg	egcatetgat	agaat catga	caggagagag	taagttttgt	6180
tctcaaaata	ccaattcctc	gaactattta	ctcagatttt	gtctgattgg	acaaggtggt	6240
trrgorttöt	tttaggtacc	tttttggtag	aatgcactga	gacagcgtca	gttcttcaga	6300
atgcaactca	ggattcacta	gtaatccttg	acgaactggg	cagaggaact	agtactttcg	6360
arggatacge	cattgcatac	toggtaacot	getattetee	ttcaacttat	acttgttgat	6430
CAACRARABC	atgcaattca	ttttgctgaa	acttattgat	ttatatoagg	tttttcgtca	6480
cctagtagag	aaaqttcaat	greggatget	ctttgcaaca	CALLACCACC	ctctcaccaa	6540

gga	acceded	rrraccesc	grgtcacctc	gaaacacatg	gottgogcat	tcaaatcaag	6500
atc	tgattat	caaccacgtg	grtgtgatca	ag acctagtg	ttettgtadd	gtttaaccga	6560
333	a gettgt	ectgagaget	acggacttca	agtggcacte	acggetggaa	taccasacca	6720
agt	ggttgaa	acagcatcag	gtgctgctca	agccatgaag	agatcaattg	gggaaaactt	6780
caa	gtcaagt	gagotaagat	ctgagttctc	aagtotgcat	dsadscrååc	tcaagtcatt	6840
ġg∶	gggtatt	totogagtog	cccacaacaa	tgcccccart	ggcgaagatg	actacgaçaç	6900
ttt	gttttgc	ttatggcatg	agatcaeatc	ctcttactgt	gttcccaaat	aaatggctat	6960
gac	âtaacac	tatctgaagc	togttaagto	ttttgcttct	ctgatgttta	ttoctottaa	7020
aab	atgetta	tatatcaaaa	aattgtttcc	tcgattataa	caagattata	tatgtatctg	7080
tcg	gtttage	tatggtatat	aatatatgta	tgttcatgag	attggtcaag	agaaatactc	7140
aca	aacagta	tattäagääg	gaaatatgtt	tatgeattaa	tttaagtttc	aagataaact	7200
â¢s	aataacc	tcgactadag	ttgcaaagac	casacacaaa	ttacaaaact	tataagaett	7260
aag	ttctgaa	ttccctaaaa	CCABBABBBB	aaacagaaca	tattttgttg	catctacaaa	7320
caa	cacaaac	ctacatagtt	tataacttac	tcatcactga	gattaacatc	agaatcattc	7380
tco	atttett	catottoact	ctcatcatca	traccaccac	catgatgatt	etectectet	7440
tca	cgtaacc	tagcastctc	actitgaget	ctatcaacaa	tetgettett	ctgcaactcc	7500
aa a	tttctct	gaaaatçagc	tctcatcttc	tccaactcct	tcatttgctc	tttcttactc	7560
ttc	tccatct	tctcataaac	CttCCCAaac	ctiticaaçaç	aateegeeaa	catcttatac	7620
gaa	gcagcgt	cattaacett	cttcctctcg	tactozacot	catcatcctc	atcctcctec	7680
tct	teagaat	caccaggact	atccatcate	teatcaaace	cattagactt	atctaaataa	7740
acc	ttagtgt	tcatasacac	aaactcacct	gaatcaacac	cacaagotaa	acctaaatcc	7800
gađ	ttgggcg	aaacacaaag	caacatatec	aacttattga	aaaacgacca	tttacttgåå	7860
cct	aaacctg	atttctcaac	cttaatcttc	tcttttctat	acttcctctt	caagtcatca	7920
atc	actotoc	tacattgcgt	ctcagatttc	tccatcetta	getecteact	cactttctca	79\$0
get	actteat	tccaatcetc	gttectcaaa	CtCCttctac	ccaattgcaa	aaacctatct	8040
ccc	CBAACTT	Caagcaacac	aa				8062

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6: C12N 15/82, 15/29, C07K 14/415, C12N 15/10, 5/04, 5/14, A01H 5/00

(11) International Publication Number: A₃

WO 99/19492

(43) International Publication Date:

22 April 1999 (22.04.99)

(21) International Application Number:

PCT/EP98/06977

(22) International Filing Date:

9 October 1998 (09.10.98)

(30) Priority Data:

PO 9745

10 October 1997 (10.10.97)

ΑU

(71) Applicant (for all designated States except US): RHONE-POULENC AGRO [FR/FR]; 14/20, rue Pierre Baizet, F-69009 Lyon (FR).

(72) Inventors; and

- (75) Inventors/Applicants (for US only): DOUTRIAUX. Marie-Pascale [FR/FR]; 64, route de Villebon, F-91160 Saulx les Chartreux (FR). BETZNER, Andreas, Stefan [AU/AU]; 40 Dallachy Place, Page, ACT 2614 (AU). FREYSSINET, Georges [FR/FR]; 21, rue de Nervieux, F-69450 Saint Cyr au Mont d'Or (FR). PEREZ, Pascal [FR/FR]; 17, chemin de la Pradelle, Varennes, F-63450 Chanonat (FR).
- (74) Agent: GENIN, Patrick; Rhône-Poulenc Agro, DPI, 14/20, rue Pierre Baizet, F-69009 Lyon (FR).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published

With international search report.

Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.

(88) Date of publication of the international search report: 24 June 1999 (24.06.99)

- (54) Title: METHODS FOR OBTAINING PLANT VARIETIES
- (57) Abstract

An isolated and purified DNA molecule comprising a polynucleotide sequence encoding a polypeptide functionally involved in the DNA mismatch repair system of a plant.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES .	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI .	Finland	LT	Lithuania	SK	Slovakia
ΑT	Austria	FR	France	LU	Luxembourg	SN	Senegal
ΑU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
ΑZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav	TM	Turkmenistan
BF	Burkina Faso	GR	Greece		Republic of Macedonia	TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	16	ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	zw	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's	NZ	New Zealand	200	Zimozowe
CM	Cameroon		Republic of Korea	PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		•
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		
				-	oPatore		
•					•		

Inte. onal Application No PCT/EP 98/06977

PCT/EP 98/06977 . CLASSIFICATION OF SUBJECT MATTER PC 6 C12N15/82 C12N IPC 6 C12N15/29 C07K14/415 C12N15/10 C12N5/04 C12N5/14 A01H5/00 According to International Patent Classification (IPC) or to both national classification and IPC **B. FIELDS SEARCHED** Minimum documentation searched (classification system followed by classification symbols) IPC 6 C12N A01H Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practical, search terms used) C. DOCUMENTS CONSIDERED TO BE RELEVANT Category * Citation of document, with indication, where appropriate, of the relevant passages Relevant to claim No. Α WO 95 15381 A (CHAPELLE ALBERT DE ;UNIV 1-5. JOHNS HOPKINS (US)) 8 June 1995 33-35 see the whole document WO 97 37011 A (SETRATECH S A R L : BORTS 1-35 RHONA HARRIET (GB); LOUIS EDWARD JOHN (GB) 9 October 1997 see abstract see the whole document A WO 90 07576 A (SETRATECH) 12 July 1990 1,7-27, 31,32 see the whole document and specially page 5, line 16-31, examples 3-4 X Further documents are listed in the continuation of box C. Patent family members are listed in annex. Special categories of cited documents: later document published after the international filing date or priomy date and not in conflict with the application but cited to understand the principle or theory underlying the "A" document defining the general state of the art which is not considered to be of particular relevance invention "E" earlier document but published on or after the international "X" document of particular relevance; the claimed invention filing date cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such docu-"O" document referring to an oral disclosure, use, exhibition or other means ments, such combination being obvious to a person skilled document published prior to the international filing date but later than the priority date claimed "&" document member of the same patent family Date of the actual completion of the international search Date of mailing of the international search report 16 April 1999 03/05/1999 Name and mailing address of the ISA Authorized officer European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nt.

1

Fax: (+31-70) 340-3016

Mateo Rosell, A.M.

onal Application No. PCT/EP 98/06977 C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT Citation of document, with indication, where appropriate, of the relevant passages Relevant to claim No. Α WO 97 01634 A (ANGELETTI P IST RICHERCHE 1.2 BIO ; JIRICNY JOSEF (IT); PALOMBO FABIO () 16 January 1997 see page 1, line 18 - page 2, line 28 see page 58 PROLLA T A ET AL: "MLH1, PMS1, AND MSH2 Α INTERACTIONS DURING THE INITATION OF DNA 1,2,4,5 MISMATCH REPAIR IN YEAST" SCIENCE. vol. 265, 19 August 1994, pages 1091-1093, XP000676403 cited in the application A. WATANABE ET AL., : "Genomic Α 1-6 organization and expresssion of the human MSH3 gene" GENOMICS. vol. 31, 1996, pages 311-318, XP002099967 see the whole document and specially Fig.3 ACHARYA S ET AL: "hMSH2 forms specific Α 1-6 mispair-binding complexes with hMSH3 and hMSH6" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, no. 93, October 1996, pages 13629- 13629, XP002080159 cited in the application sequences from this paper deposited in GenBank under AC= U61981 (hMSH3), and U54777 and U73732-7 (hMSH6). see the whole document K. LIU ET AL., : "characterization of the Α 1-6 mouse Rep-3 gene: sequence similarities to bacterial and yeast mismatch-repair proteins" GENE, vol. 147, 1994, pages 169-177, XP002099968 see the whole document and specially Figure 2. Α I. IACCARINO ET AL., : "MSH6, a 1-6 Saccharomyces cerevisiae protein that binds to mismatches as a heterodimer with MSH2" CURRENT BIOLOGY, vol. 6, no. 4, April 1996, pages 484-486, XP002099969 sequence is deposited at GenBank under AC= Z47746. see the whole document -/--

1

Inte onal Application No
PCT/EP 98/06977

C (Carrier		PCT/EP 9	8/069//
Category '	ation) DOCUMENTS CONSIDERED TO BE RELEVANT Citation of document, with indication, where appropriate, of the relevant passages		[Selevento et
	appropriate, or the relevant passages		Relevant to claim No.
Α	CORRADI A ET AL: "CDNA SEQUENCE, MAP, AND EXPRESSION OF THE MURINE HOMOLOG OF GTBP, ADNA MISMATCH REPAIR GENE" GENOMICS, vol. 36, no. 2, 1 September 1996, pages 288-295, XP000613761 see the whole document and specially Fig.1		1-6
P,X	DATABASE EMBL NUCLEOTIDE AND PROTEIN SEQUENCES,13 July 1998, XP002099368 HINXTON, GB AC= AJ007791. Arabidopsis thaliana mRNA for mismatch repair protein (MSH3) see abstract		1-6
P,X	DATABASE EMBL NUCLEOTIDE AND PROTEIN SEQUENCES,1 August 1998, XP002099369 HINXTON, GB AC= 065607. Arabidopsis thaliana. Putative mismacht DNA repair protein see abstract		1-5
P,X .	DATABASE EMBL NUCLEOTIDE AND PROTEIN SEQUENCES,16 October 1997, XP002099371 HINXTON, GB AC= AF009657. Arabidopsis thalian MutS homolog 6-like protein mRNA. see abstract -& K.M. CULLIGAN AND J.B. HAYS: "DNA mismatch repair in plants" PLANT PHYSIOLOGY, vol. 115, 1997, pages 833-839, XP002099372 see the whole document		1-6
	DATABASE EMBL NUCLEOTIDE AND PROTEIN SEQUENCES,17 December 1998, XP002099373 HINXTON, GB AC= AJ131669. Triticum aestivum mRNA for MSH3 protein, MSH3 gene. see abstract		1-6
	DATABASE EMBL NUCLEOTIDE AND PROTEIN SEQUENCES,12 October 1998, XP002099370 HINXTON, GB AC= AJ007792. Arabidopsis thaliana DNA mismatch repair protein, MSH6 gene. see abstract		1-6

1 .

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

Information on patent f			mation on patent family members	ily members			PCT/EP 98/06977	
	tent document in search report		Publication date	Patent family member(s)			Publication date .	
WO	9515381	A	08-06-1995	EP JP US US	073064 950650 569347 583744	9 T 0 A	11-09-1996 30-06-1997 02-12-1997 17-11-1998	
WO	9737011	Α	09-10-1997	NON	E			
WO	9007576	A	12-07-1990	FR AT AU CA DE DE EP ES IE JP	264179 12751 483439 200654 6892417 6892417 044992 207705 7246 450360	9 T 00 A 9 A 4 D 4 T 3 A 8 T 9 B	20-07-1990 15-09-1995 01-08-1990 26-06-1990 12-10-1995 14-03-1996 09-10-1991 16-11-1995 09-04-1997 02-07-1992	
WO	9701634	Α	16-01-1997	IT AU	RM95043 624129		27-12-1996 30-01-1997	